

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	329	100.0	332	12	AD122022	Ad122022	Maize 3'
2	329	100.0	1236	13	ADXP30934	AdXP30934	Plant full
3	329	100.0	5118	12	ADP73930	AdP73930	Plasmid p
4	329	100.0	7545	10	ACF58343	AcF58343	Nucleotid
5	329	100.0	11643	10	ACF58344	AcF58344	Nucleotid
6	329	100.0	13680	12	ADP73931	AdP73931	Plasmid p
7	327.4	99.5	1206	13	ADK61274	AdK61274	Plant full
8	327.4	99.5	1271	13	ADX10934	AdX10934	Plant full
9	316.4	96.2	725	13	ADX10594	AdX10594	Plant full
10	315	95.7	526	13	ADX10536	AdX10536	Plant full
11	304	91.6	1294	13	ADT17732	AdT17732	Plant cDN
12	294	89.4	1057	13	ADO83213	AdO83213	Plant full
13	286	86.9	818	13	ADK65031	AdK65031	Plant full
14	278.4	84.6	458	13	ADX10617	AdX10617	Plant full
15	278.4	84.6	1216	13	ADX50588	AdX50588	Plant full
16	235.4	71.6	1594	13	ADK65204	AdK65204	Plant full
17	232.6	70.7	1234	13	ADX50026	AdX50026	Plant full
18	232.6	70.7	1278	13	ADK52932	AdK52932	Plant full
19	204	62.0	1057	13	ADO84166	AdO84166	Plant full

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	329	100.0	332	12	AD122022	Maize 3'
2	329	100.0	1236	13	ADX120934	Plant ful
3	329	100.0	5118	12	ADP73930	Adx73930 Plasmid p
4	329	100.0	7545	10	ACF58343	Act58343 Nucleotid
5	329	100.0	11643	10	ACF58344	Act58344 Nucleotid
6	329	100.0	13680	12	ADP73931	Adx73931 plasmid p
7	327.4	99.5	1206	13	ADX61274	Adx61274 Plant ful
8	327.4	99.5	1271	13	ADX10934	Adx10934 Plant ful
9	316.4	96.2	725	13	ADX10594	Adx10594 Plant ful
10	315	95.7	526	13	ADX10536	Plant ful
11	301.4	91.6	1294	13	ADT17732	Plant cDN
12	294	89.4	1057	13	ADX83213	Plant ful
13	286	86.9	818	13	ADX65031	Plant ful
14	278.4	84.6	458	13	ADX10617	Plant ful
15	278.4	84.6	1216	13	ADX50588	Plant ful
16	235.4	71.6	1294	13	ADX65204	Plant ful
17	232.6	70.7	1234	13	ADX50026	Plant ful
18	232.6	70.7	1278	13	ADX52932	Plant ful
19	204	62.0	1057	13	ADX084166	Plant ful

RESULT 1
ADI22022
ID ADI22022 standard; DNA; 332 BP.

22-APR-2004 (first entry)

Maize 3' UTR.

ss; 3' untranslated region ; UTR; expression cassette ;
 KW transformed plant; promoter ; untranslated leader sequence;
 KW genetic engineering.

XX
OS
Zea mays

XX
PN
W02004003177-A2

XX
08-JAN-2004
RDXX
PF 25-TTN-2003-2003WO-TIS020977

27-JUN-2002 2002US-0392571P

XX
PA (DOWC) DOW AGROSCIENTES I.L.C

XX
PT Cowen NM Smith KA Armstrong K.

WPT: 2004-071986/07

New isolated DNA molecule useful for genetic engineering of plants or for improving the expression of transgenes in plants, particularly corn plants

XX
PC
Claim 1. GEO TD NO 1. 30mm. English

This sequence represents a 3' untranslated region (UTR) which was used in the construction of the recombinant expression cassette of the invention. The expression cassette is for effecting expression of a foreign gene in a transformed plant and comprises a promoter operable in plants, an untranslated leader sequence, a foreign gene of interest, and a 3'UTR. This cassette may be used to transform plants for genetic engineering of

CC plants or in improving the expression of transgenes in plants.

XX
SQ Sequence 332 BP; 51 A; 62 C; 100 G; 116 T; 0 U; 3 Other;
Query Match 100.0%; Score 329; DB 12; Length 332;
Best Local Similarity 100.0%; Pred. No. 7e-91;
Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTCCAGCGTGTGGTGTGCGTGTGCTGTGCTGTGCGCGCGCGCGCGCGCGATC 60
DB 1 GGTCCAGCGTGTGGTGTGCGTGTGCTGTGCTGTGCGCGCGCGCGCGCGCGATC 60
QY 61 AGAANCCTTGGCTGGCGGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 120
DB 61 AGAANCCTTGGCTGGCGGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 120
QY 121 CAAAGTGATCGCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 180
DB 121 CAAAGTGATCGCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 180
QY 181 GGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 240
DB 181 GGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 240
QY 241 ACTACTTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 300
DB 241 ACTACTTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 300
QY 301 TGGACATGTTATGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 332
DB 301 TGGACATGTTATGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 332

RESULT 2

ADX30934
ID ADX30934 standard; cDNA; 1236 BP.

XX
AC ADX30934;

XX
DT 21-APR-2005 (first entry)

XX
DE Plant full length insert polynucleotide seqid 13754.

XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.

XX
OS Unidentified.

XX
PN US2004034888-A1.

XX
PD 19-FEB-2004.

XX
PF 28-APR-2003; 2003US-00425114.

XX
PR 06-MAY-1999; 99US-00304517.

XX
PR 05-NOV-2001; 2001US-00985678.

XX
PA (LIU//) LIU J.

XX
PA (ZHOU//) ZHOU Y.

XX
PA (KOVA//) KOVALIC D K.

XX
PA (SCRE//) SCREEN S E.

XX
PA (TAB//) TABASKA J E.

XX
PA (CAO//) CAO Y.

XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.

XX

PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.

XX
PS Claim 1; SEQ ID NO 13754; 15pp; English.

XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.

XX
SQ Sequence 1236 BP; 288 A; 333 C; 405 G; 210 T; 0 U; 0 Other;

Query Match 100.0%; Score 329; DB 13; Length 1236;
Best Local Similarity 99.1%; Pred. No. 1.2e-90;
Matches 329; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTCCAGCGTGTGGTGTGCGTGTGCTGTGCTGTGCGCGCGCGCGCGCGATC 60
DB 897 GGTCCAGCGTGTGGTGTGCGTGTGCTGTGCTGTGCGCGCGCGCGCGCGATC 956
QY 61 AGAANCCTTGGCTGGCGGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 120
DB 957 AGAANCCTTGGCTGGCGGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1016
QY 121 CAAAGTGATCGCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 180
DB 1017 CAAAGTGATCGCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1076
QY 181 GTGTTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 240
DB 1077 GTGTTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1136
QY 241 ACTACTTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 300
DB 1137 ACTACTTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 1196
QY 301 TGGACATGTTATGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 332
DB 1197 TGGACATGTTATGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1228

RESULT 3

ADP73930

ID ADP73930 standard; DNA; 5118 BP.

XX
AC ADP73930;

XX
DT 09-SEP-2004 (first entry)

XX
DE Plasmid pDAB3014, SEQ ID NO:84.

XX
KW Transgenic plant; immunoglobulin production; recombinant production;
KW glycosylation; fucose; glycan; virucide; immunotherapy; maize; lipase;
KW 3'UTR; rice; actin promoter; phosphinothricin acyltransferase; PAT;
KW plasmid; pDAB3014; cyclic; circular; ds.

OS Zea mays.
 OS Oryza sativa.
 OS Chimeric.
 OS Unidentified.
 XX Key
 FT promoter
 FT 1172..1724
 FT /tag= a
 FT /notes= "Rice actin promoter"
 FT 1727..2281
 FT /tag= b
 FT /product= "Phosphinothricin acyltransferase (PAT)"
 FT 2296..2627
 FT /tag= c
 FT /note= "Maize lipase 3'UTR. The 3' end of this 3'UTR has
 FT been deduced from that given for pDAB8505 (SEQ ID NO:85),
 FT as the 3'UTR location given for this plasmid is 2296-
 FT 6652"
 XX WO2004050838-A2.
 XX 17-JUN-2004.
 XX 28-NOV-2003; 2003WO-US037905.
 XX 27-NOV-2002; 2002US-0429385P.
 XX (DOWC) DOW CHEM CO.
 XX (DOWC) DOW AGROSCIENCES LLC.
 XX (EPIC-) EPICYTE PHARM INC.
 XX Briggs K, Glancy T, Hein MB, Hiatt AC, Karnoup AL, Anderson WHK;
 PI Pareddy D, Petolino J, Rubin-Wilson B, Taylor D, Roberts JL;
 XX WPI; 2004-461111/43.
 XX Novel plant-produced immunoglobulin having glycopeptide or glycan profile
 PT with reduced fucosylation, useful for treating herpes simplex virus
 PT infection.
 XX Claim 69; SEQ ID NO 84; 212pp; English.
 XX The invention relates to the production of immunoglobulins in plants,
 CC wherein at least a portion of the glycans attached to the immunoglobulins
 CC lack fucose. The immunoglobulins produced can be of any class (i.e., IgG,
 CC IgA, IgM, IgE or IgD) and is especially an anti-herpes simplex virus
 CC (HSV) antibody or an anti-alpha/beta3, alpha/beta5 dual integrin
 CC antibody. The invention also relates to constructs, plasmids and vectors
 CC for producing the immunoglobulins; transformed plant cells, calli, plant
 CC tissues and whole plants for producing the immunoglobulins; methods for
 CC producing the immunoglobulins, the immunoglobulins thus produced; and the
 CC use of such immunoglobulins. The immunoglobulins of the invention may be
 CC used to treat HSV infection or tumour angiogenesis. The invention
 CC provides the advantages of antibody production in plants, such as large
 CC scale production, reduced costs, and elimination of pathogenic
 CC contaminants such as viruses and prions, with a simplified (i.e., non-
 CC plant-specific) glycosylation profile which reduces the risk that the
 CC immunoglobulin may not be functional in animals. The present sequence
 CC represents the plasmid pDAB3014, which may be used in the invention. The
 CC plasmid contains a phosphinothricin acyltransferase (PAT) gene under the
 CC control of a rice actin promoter, and a maize lipase 3'UTR.
 XX Sequence 5118 BP; 1240 A; 1256 C; 1286 G; 1336 T; 0 U; 0 Other;
 Query Match 100.0%; Score 329; DB 12; Length 5118;
 Best Local Similarity 99.1%; Pred. NO. 2.1e-90;
 Matches 329; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 1 GGTCCGACGGTGTGCGTCCGTCGTACGTTCTGGCGCGCGCGCTTGGCGCGCGATC 60
 2296 GGTCCGACGGTGTGCGTCCGTCGTACGTTCTGGCGCGCGCGCTTGGCGCGCGATC 2355

QY 61 AGAANCCTTGGTGGCGTGTGTGCTTCTGCTTTGCTTTAAATTTTACCAAGTTTGT 120
 DB 2356 AGAAGCGTTGGTGGCGTGTGTGCTTCTGCTTTGCTTTAAATTTTACCAAGTTTGT 2415
 QY 121 CAAGGTGGATCGCGTGGTCAAGGCCCGGTGTGTCTTTAAANACCCACCGGCACTGGCAGTGA 180
 DB 2416 CAAGGTGGATCGCGTGGTCAAGGCCCGGTGTGTCTTTAAAGACCCACCGGCACTGGCAGTGA 2475
 QY 181 GTGTTGCTGCTGTGTAGGCTTTGTAGTATGAGCTTTATTTGCTTCTGGATGTTGTGT 240
 DB 2476 GTGTTGCTGCTGTGTAGGCTTTGTAGTATGAGCTTTATTTGCTTCTGGATGTTGTGT 2535
 QY 241 ACTACTCTGGTGTGTGAATTTATTTATGATGAGCTTTGCTTCTGGATGTTGTGT 300
 DB 2536 ACTACTCTGGTGTGTGAATTTATTTATGAGCTTTGCTTCTGGATGTTGTGT 332
 QY 301 TGGACATTTGTTATGTTATTAATAAATGCTTTTGC 332
 DB 2596 TGGACATTTGTTATGTTATTAATAAATGCTTTTGC 2627
 RESULT 4
 ACF58343
 ID ACF58343 standard; DNA; 7545 BP.
 XX AC ACF58343;
 XX 12-FEB-2004 (first entry)
 XX Nucleotide sequence of plasmid pDAB8504.
 XX GntIII; N-acetylglucosaminyltransferase; transgenic; glycoprotein; ds.
 XX Synthetic.
 XX Key
 FT Location/Qualifiers
 FT misc_feature
 FT 1..1146
 FT /tag= a
 FT /note= "tobacco Rb7 MARs"
 FT 1167..1304
 FT /tag= b
 FT /note= "linker sequence (ACF58351)"
 FT 1305..2701
 FT /tag= c
 FT /note= "rice actin promoter and intron"
 FT 2235..2696
 FT /tag= d
 FT /note= "rice actin intron"
 FT 2704..3258
 FT /tag= e
 FT /note= "PAT gene"
 FT 3259..3272
 FT /tag= f
 FT /note= "linker sequence (ACF58352)"
 FT 3273..3629
 FT /tag= g
 FT /note= "maize lipase UTR"
 FT complement(3671..4836)
 FT /tag= i
 FT /note= "tobacco Rb7 MAR"
 FT 4351..4405
 FT /tag= h
 FT /note= "linker sequence (ACF58353)"
 FT 4837..4857
 FT /tag= j
 FT /note= "linker sequence (ACF58354)"
 FT 4858..5103
 FT /tag= k
 FT /note= "Puc19"
 FT 5104..5130
 FT /tag= l
 FT /note= "linker sequence (ACF58355)"
 FT 5130..7523

```
FT      /*tag= m
FT      /note= "Puc19"
FT      misc_feature 7524..7545
FT      /*tag= n
FT      /note= "linker sequence (ACF58356)"
XX
XX WO2003078614-A2.
XX
XX 25-SEP-2003.
XX
XX 18-MAR-2003; 2003WO-IB001562.
XX
XX 19-MAR-2002; 2002US-0365769P.
XX 26-MAR-2002; 2002US-0368047P.
XX
XX (PLAN-) PLANT RES INT BV.
XX
XX Bakker HAC, Florack DEA, Bosch HJ;
XX
XX WPI; 2003-779132/73.
XX
XX New plant host cell system for producing a desired glycoprotein comprises
XX a mammalian N-acetylglucosaminyltransferase (GnTIII) enzyme, a nucleic
XX acid sequence encoding the enzyme, or a vector comprising the nucleic
XX acid sequence.
XX
XX Example 6; Fig 7B; 122pp; English.
XX
XX The invention relates to a plant host cell system comprising a mammalian
XX UDP-N-acetylglucosamine: beta-D mannose beta(1,4)-N-
XX acetylglucosaminyltransferase (GnTIII) enzyme, a nucleic acid sequence
XX encoding a mammalian GnTIII protein, or a vector comprising the GnTIII
XX nucleic acid. The plant host system is useful in producing a desired
XX glycoprotein or its functional fragment. The glycoprotein or its
XX functional fragment may be used for the production of a pharmaceutical
XX composition. The present sequence represents the nucleotide sequence of
XX plasmid pDAB8504
XX
XX Sequence 7545 BP; 2128 A; 1579 C; 1622 G; 2216 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 329; DB 10; Length 7545;
XX Best Local Similarity 99.1%; Pred. No. 2.4e-90;
XX Matches 329; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGTCCAGCGTGTGCGTCCGTCGTCTGCTGCGCGCGCGCGCTTGGCGCGCGATC 60
Db |||||
3273 GGTCCAGCGTGTGCGTCCGTCGTCTGCTGCGCGCGCGCGCTTGGCGCGCGATC 3332
QY 61 AGAANCCTTGGCTTGGCGTGTGCTGCTTCTGCTTAAATTTTACCAAGTTTGT 120
Db |||||
3333 AGAAGCTTGGCTTGGCGTGTGCTGCTTCTGCTTAAATTTTACCAAGTTTGT 3392
QY 121 CAAGTGGATCCGCTGCAAGCCCGTGTGCTTTAAANACCACCGGCACTGGCAGTGA 180
Db |||||
3393 CAAGTGGATCCGCTGCAAGCCCGTGTGCTTTAAAGACCCACCGGCACTGGCAGTGA 3452
QY 181 GGTGTGCTGCTGTGCTGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 240
Db |||||
3453 GGTGTGCTGCTGTGCTGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 3512
QY 241 ACTACTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 300
Db |||||
3513 ACTACTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 3572
QY 301 TGGACATTTGTTATGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 332
Db |||||
3573 TGGACATTTGTTATGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3604
XX
XX RESULT 5
XX ACF58344
XX ID ACF58344 standard; DNA; 11643 BP.
XX
```

```
AC ACF58344;
XX
XX 12-FEB-2004 (first entry)
XX
XX Nucleotide sequence of plasmid pDAB7113.
XX
XX GnTIII; N-acetylglucosaminyltransferase; transgenic; glycoprotein; ds.
XX
XX Synthetic.
XX
XX Key
XX Location/Qualifiers
XX 1..1164
XX misc_feature
XX /*tag= a
XX /note= "Rb7 MAR v3"
XX
XX 1165..1233
XX misc_feature
XX /*tag= b
XX /note= "linker sequence (ACF58357)"
XX
XX 1234..3224
XX promoter
XX /*tag= c
XX /note= "maize ubiquitin 1 promoter"
XX
XX 3225..4891
XX misc_feature
XX /*tag= d
XX /note= "GNTIII v.2"
XX
XX 4896..5260
XX 3'UTR
XX /*tag= e
XX /note= "maize peroxidase-5 3'-UTR"
XX
XX 5261..5404
XX misc_feature
XX /*tag= f
XX /note= "multiple cloning sites (ACF58358)"
XX
XX 5405..6802
XX promoter
XX /*tag= g
XX /note= "rice actin 1 promoter v2"
XX
XX 6803..7358
XX misc_feature
XX /*tag= h
XX /note= "PAT v3"
XX
XX 7359..7372
XX misc_feature
XX /*tag= i
XX /note= "linker sequence (ACF58359)"
XX
XX 7373..7729
XX 3'UTR
XX /*tag= j
XX /note= "maize lipase UTR"
XX
XX 7730..7770
XX misc_feature
XX /*tag= k
XX /note= "linker sequence (ACF58360)"
XX
XX 7771..8934
XX misc_feature
XX /*tag= l
XX /note= "Rb7 MAR v3"
XX
XX 8935..11643
XX misc_feature
XX /*tag= m
XX /note= "Puc19"
XX
XX 10164..11021
XX misc_feature
XX /*tag= n
XX /note= "ampicillin resistance gene"
XX
XX WO2003078614-A2.
XX
XX 25-SEP-2003.
XX
XX 18-MAR-2003; 2003WO-IB001562.
XX
XX 19-MAR-2002; 2002US-0365769P.
XX 26-MAR-2002; 2002US-0368047P.
XX
XX (PLAN-) PLANT RES INT BV.
XX
XX Bakker HAC, Florack DEA, Bosch HJ;
XX
XX WPI; 2003-779132/73.
XX
XX New plant host cell system for producing a desired glycoprotein comprises
XX a mammalian N-acetylglucosaminyltransferase (GnTIII) enzyme, a nucleic
XX acid sequence encoding the enzyme, or a vector comprising the nucleic
XX acid sequence.
```



```
XX Claim 69; SEQ ID NO 85; 212pp; English.
PS
XX
CC The invention relates to the production of immunoglobulins in plants,
CC wherein at least a portion of the glycans attached to the immunoglobulins
CC lack fucose. The immunoglobulins produced can be of any class (i.e., IgG,
CC IgA, IgM, IgE or IgD) and is especially an anti-herpes simplex virus
CC (HSV) antibody or an anti-alphaVbeta3, alphaVbeta5 dual integrin
CC antibody. The invention also relates to constructs, plasmids and vectors
CC for producing the immunoglobulins; transformed plant cells, calli, plant
CC tissues and whole plants for producing the immunoglobulins; methods for
CC producing the immunoglobulins, the immunoglobulins thus produced; and the
CC use of such immunoglobulins. The immunoglobulins of the invention may be
CC used to treat HSV infection or tumour angiogenesis. The invention
CC provides the advantages of antibody production in plants, such as large
CC scale production, reduced costs, and elimination of pathogenic
CC contaminants such as viruses and prions, with a simplified (i.e., non-
CC plant-specific) glycosylation profile which reduces the risk that the
CC immunoglobulin may not be functional in animals. The present sequence
CC represents the plasmid pDAB8505, which contains codon optimised DNA
CC sequences encoding the heavy and light chains of the human anti-HSV1/HSV2
CC monoclonal IgA antibody HX8 each of which are fused to mouse leader
CC sequences. Both heavy and light chain fusion genes are under the control
CC of maize endosperm-specific gamma-zin promoters. The plasmid also
CC contains a phosphinothricin acyltransferase (PAT) gene under the control
CC of a rice actin promoter.
XX
SQ Sequence 13680 BP; 3886 A; 3069 C; 2934 G; 3788 T; 0 U; 3 Other;
Query Match 100.0%; Score 329; DB 12; Length 13680;
Best Local Similarity 100.0%; Pred. No. 3.1e-90;
Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTCCAGCGTGTGGTGTCCGTGTACGTTCTGCGCGCGCGGCTTGGGCGCGCATC 60
DB 9831 GGTCCAGCGTGTGGTGTCCGTGTACGTTCTGCGCGCGCGGCTTGGGCGCGCATC 9890
QY 61 AGAANCCTGCTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 9891 AGAANCCTGCTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9950
QY 121 CAAGGTGGATCGCGTGTGCAAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 9951 CAAGGTGGATCGCGTGTGCAAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 10010
QY 181 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 10011 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 10070
QY 241 ACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 10071 ACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 10130
QY 301 TGGACATGTTATGTTATTAATAAATGCTTTGC 332
DB 10131 TGGACATGTTATGTTATTAATAAATGCTTTGC 10162
RESULT 7
ADX61274
ID ADX61274 standard; cDNA; 1206 BP.
XX
XX ADX61274;
XX
XX 21-APR-2005 (first entry)
XX
XX Plant full length insert polynucleotide seqid 32117.
XX
XX plant protectant; plant growth regulant; gene therapy; plant;
XX recombinant DNA construct; physical array; plant breeding marker;
XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX extreme osmotic condition; pathogen tolerance; pest tolerance;
XX growth rate; cell cycle pathway; disease resistance;
```

```
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX
XX Unidentified.
OS
XX US2004034888-A1.
PN
XX 19-FEB-2004.
PD
XX 28-APR-2003; 2003US-00425114.
PF
XX 06-MAY-1999; 99US-00304517.
PR
XX 05-NOV-2001; 2001US-00985678.
PX
XX (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TAB/) TABASKA J E.
PA (CAOY/) CAO Y.
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX pests, for conferring increased resistance to plant disease, or for
XX improving yield.
PS Claim 1; SEQ ID NO 32117; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
XX of the invention are also useful in physical arrays of molecules and as
XX plant breeding markers. The recombinant DNA construct is useful for
XX improving plant tolerance to cold, heat, drought, herbicides, extreme
XX osmotic conditions, pathogens or pests, for manipulating growth rate in
XX plant cells by modification of the cell cycle pathway, for conferring
XX increased resistance to plant disease, for producing galactomannan,
XX lignin or plant growth regulators, for increasing the rate of homologous
XX recombination in plants, for improving yield by modification of
XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX or by providing improved plant growth and development under at least one
XX stress condition or for modifying seed oil or protein yield and/or
XX content. This sequence represents a plant full length insert
XX polynucleotide that can be used in the recombinant DNA construct of the
XX invention.
SQ Sequence 1206 BP; 281 A; 337 C; 395 G; 193 T; 0 U; 0 Other;
Query Match 99.5%; Score 327.4; DB 13; Length 1206;
Best Local Similarity 98.8%; Pred. No. 3.6e-90;
Matches 328; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GGTCCAGCGTGTGGTGTCCGTGTACGTTCTGCGCGCGCGGCTTGGGCGCGCATC 60
DB 867 GGTCCAGCGTGTGGTGTCCGTGTACGTTCTGCGCGCGCGGCTTGGGCGCGCATC 926
QY 61 AGAANCCTGCTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 927 AGAANCCTGCTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 986
QY 121 CAAGGTGGATCGCGTGTGCAAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 987 CAAGGTGGATCGCGTGTGCAAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1046
QY 181 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 1047 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1106
```

QY 241 ACTACTGGGTTGTTGAATTATTATGACAGTTGGCTATTGTAATTCAGCTGGGCTACC 300
|||||
Db 1107 ACTACTGGGTTGTTGAATTATTATGAGCAGTTGGCTATTGTAATTCAGCTGGGCTACC 1166
|||||
QY 301 TGGACATTGTTATGTTAATTAATAATGCTTTGC 332
|||||
Db 1167 TGGACATTGTTATGTTAATTAATAATGCTTTGC 1198
|||||

RESULT 8

ADX10934
ID ADX10934 standard; cDNA; 1271 BP.

AC ADX10934;

DT 21-APR-2005 (first entry)

DE Plant full length insert polynucleotide seqid 5509.

XX plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.

XX Unidentified.

XX US2004034888-A1.

XX 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

XX 05-NOV-2001; 2001US-00985678.

XX (LIUJ/) LIU J.

XX (ZHOU/) ZHOU Y.

XX (KOVA/) KOVALIC D K.

XX (SCRE/) SCREEN S E.

XX (TABA/) TABASKA J E.

XX (CAOY/) CAO Y.

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to

PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.

XX Claim 1; SEQ ID NO 5509; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or

CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.

XX Sequence 1271 BP; 295 A; 350 C; 412 G; 214 T; 0 U; 0 Other;

QY Query Match 99.5%; Score 327.4; DB 13; Length 1271;

XX Best Local Similarity 98.8%; Pred. No. 3.7e-90;

XX Matches 328; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGTGCGAGCGTGTGGCTGTCCTGCTACGTTCTGCGCGCGCGGCTTGGCGCGCGGATC 60
|||||

Db 932 GGTGCGAGCGTGTGGCTGTCCTGCTACGTTCTGCGCGCGCGGCTTGGCGCGCGGATC 991
|||||

QY 61 AGAANGCTTGGCTTGGCGGTGTGCTTCTGCTTAAATTTTACCAAGTTTGT 120
|||||

Db 992 AGAAGCGTTGCGTGGCGGTGTGCTTCTGCTTAAATTTTACCAAGTTTGT 1051
|||||

QY 121 CAAGCTGGATCGCGTGTCAAGGCCGCTGTCTTTAAACCCACCGGCACTGGCAGTGA 180
|||||

Db 1052 CAAGCTGGATCGCGTGTCAAGGCCGCTGTCTTTAAACCCACCGGCACTGGCAGTGA 1111
|||||

QY 181 GTGTTGCTGCTTGTGTAGCTTTGCTATGCTATGCTTCTTCTGGAATGTTGCT 240
|||||

Db 1112 GTGTTGCTGCTTGTGTAGCTTTGCTATGCTATGCTTCTTCTGGAATGTTGCT 1171
|||||

QY 241 ACTACTGGGTTTGTGAATTATTATGACAGTTGGCTATTGTAATTCAGCTGGGCTACC 300
|||||

Db 1172 ACTACTGGGTTTGTGAATTATTATGACAGTTGGCTATTGTAATTCAGCTGGGCTACC 1231
|||||

QY 301 TGGACATTGTTATGTTAATTAATAATGCTTTGC 332
|||||

Db 1232 TGGACATTGTTATGTTAATTAATAATGCTTTGC 1263
|||||

RESULT 9

ADX10594

ID ADX10594 standard; cDNA; 725 BP.

XX AC ADX10594;

XX 21-APR-2005 (first entry)

XX Plant full length insert polynucleotide seqid 5169.

XX plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.

XX Unidentified.

XX US2004034888-A1.

XX 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

XX 05-NOV-2001; 2001US-00985678.

XX (LIUJ/) LIU J.

XX (ZHOU/) ZHOU Y.

XX (KOVA/) KOVALIC D K.

XX (SCRE/) SCREEN S E.

XX (TABA/) TABASKA J E.

XX (CAOY/) CAO Y.

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX PI

XX WPI; 2004-180133/17.
DR New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX
PS Claim 1; SEQ ID NO 5169; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.secdatas.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 725 BP; 149 A; 205 C; 226 G; 145 T; 0 U; 0 Other;
Query Match 96.2%; Score 316.4; DB 13; Length 725;
Best Local Similarity 98.8%; Pred. No. 7.2e-87;
Matches 317; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GGTCCAGCGTGTGGTGTCCGTCTAGCTTCTGCGCGCGCGCTTGGGCGCGCATC 60
DB 405 GGTCCAGCGTGTGGTGTCCGTCTAGCTTCTGCGCGCGCGCTTGGGCGCGCATC 464
QY 61 AGAANCCTGGTGGTGGTGTGTGTCTGTGGTCTTTAAATTTTACCAAGTTTGT 120
DB 465 AGAAGCGTTGGTGGTGGTGTGTGTCTGTGGTCTTTAAATTTTACCAAGTTTGT 524
QY 121 CAAGGTGATCGCGTGTCAAGCGCGTGTCTTTAAANACCCACCGCATGCACTGA 180
DB 525 CAAGGTGATCGCGTGTCAAGCGCGTGTCTTTAAANACCCACCGCATGCACTGA 584
QY 181 GTGTGTCTGT 240
DB 585 GTGTGTCTGT 644
QY 241 ACTACTGGT 300
DB 645 ACTACTGGT 704
QY 301 TGGACATTTTATGATTAAT 321
DB 705 TGGACATTTTATGATTAAT 725

RESULT 10
ADX10536
ID ADX10536 standard; cDNA; 526 BP.
XX
AC ADX10536;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 5111.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
XX protein content; gene; ss.
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
XX
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
XX (CAOY/) CAO Y.
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
DR
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 5111; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.secdatas.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 526 BP; 95 A; 134 C; 169 G; 128 T; 0 U; 0 Other;

Query Match 95.7%; Score 315; DB 13; Length 526;
Best Local Similarity 99.1%; Pred. No. 1.7e-86;
Matches 315; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGTCCAGCGTGTGGTGTCCGTCTAGCTTCTGCGCGCGCGCTTGGGCGCGCATC 60
DB 209 GGTCCAGCGTGTGGTGTCCGTCTAGCTTCTGCGCGCGCGCTTGGGCGCGCATC 268
QY 61 AGAANCCTGGTGGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
DB 269 AGAAGCGTTGGTGGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 328
QY 121 CAAGGTGATCGCGTGTCAAGCGCGTGTCTTTAAANACCCACCGCATGCACTGA 180
DB 329 CAAGGTGATCGCGTGTCAAGCGCGTGTCTTTAAAGACCCACCGCATGCACTGA 388
QY 181 GTGTGTCTGT 240

QY 58 ATCAAGACGCTTCGCTGGCGTGTGCTGCTTCTGCTTTAATTTTACCAAGTTTG 117
 |||||
 Db 521 ATCAGAAGCGTTCGCTGGCGTGTGCTGCTTCTGCTTTAATTTTACCAAGTTTG 580
 |||||
 QY 118 TTTCAGAGTGATCGCTGCTCAAGCCCGCTGCTTTAAANACCCACCGGCACTGGCAG 177
 |||||
 Db 581 TTTCAGAGTGATCGCTGCTCAAGCTTCGCTTTAAAGACCCACCGGCACTGGCAG 640
 |||||
 QY 178 TGAGTCTGCTGCTGTAGGCTTTGGTACGTATCGGCTTTAATTTGCT----- 226
 |||||
 Db 641 TCAGTCTGCTGCTGTAGGCTTTGGTACGTATCGGCTTTAATTTGCTTCTAAGTCAGG 700
 |||||
 QY 227 -TCTGATGCTGTGCTACTTCTGGCTTCTGCTTTAATTTATGACAGTTGCGTATTGTAA 285
 |||||
 Db 701 GTCGTGATGCTGTGCTACTTCTGGCTTCTGCTTTAATTTATGACAGTTGCGTATTGTAA 760
 |||||
 QY 286 TTCAGCTGGGCTACCTGGACATTTGTTATGTTAATTAATAATGCTTTGCG 332
 |||||
 Db 761 TTCAGCTGGGCTACCTGGACATTTGTTATGTTAATTAATAATGCTTTGCG 807
 |||||

RESULT 14

ADX10617
 ID ADX10617 standard; cDNA; 458 BP.

XX AC ADX10617;

XX DT 21-APR-2005 (first entry)

XX DE Plant full length insert polynucleotide seqid 5192.

XX KW plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content; gene; ss.

XX OS Unidentified.

XX PN US2004034888-A1.

XX PD 19-FEB-2004.

XX PF 28-APR-2003; 2003US-00425114.

XX PR 06-MAY-1999; 99US-00304517.

XX PR 05-NOV-2001; 2001US-00985678.

XX PA (LIUJ/) LIU J.

XX PA (ZHOU/) ZHOU Y.

XX PA (KOVA/) KOVALIC D'K.

XX PA (SCRE/) SCREEN S E.

XX PA (TABA/) TABASKA J E.

XX PA (CAOY/) CAO Y.

XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX XX WPI; 2004-180133/17.

XX DR New recombinant DNA construct, useful for improving plant tolerance to

XX PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.

XX PS Claim 1; SEQ ID NO 5192; 15pp; English.

XX CC The invention describes a recombinant DNA construct comprising a

CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at

CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide

CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.

XX SQ Sequence 458 BP; 80 A; 115 C; 149 G; 114 T; 0 U; 0 Other;

Query Match 84.6%; Score 278.4; DB 13; Length 458;

Best Local Similarity 98.6%; Pred. No. 38-75;

Matches 279; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGTGCGAGCGTGTGCGTGTCCGTGCTGCTGCTTCTGCGCGCGGCGCTTGGCGCGGATC 60

Db 176 GGTGCGAGCGTGTGCGTGTCCGTGCTGCTGCTTCTGCGCGCGGCGCTTGGCGCGGATC 235

QY 61 AGAANCGTTGCGTTGGCGGTGTGCTGCTTCTGCTTCTTAAATTTTACCAAGTTTGT 120

Db 236 AGAAGCGTTGCGTTGGCGGTGTGCTGCTTCTGCTTCTTAAATTTTACCAAGTTTGT 295

QY 121 CAAAGTGATCCGCTGCTCAAGCCCGCTGCTGCTTAAANACCCACCGGCACTGGCAGTGA 180

Db 296 CAAAGTGATCCGCTGCTCAAGCTCGCTGCTGCTTAAAGACCCACCGGCACTGGCAGTGA 355

QY 181 GGTGCTGCTTGTGCTGCTGCTTGTGCTGCTGCTGCTTGTGCTTCTGCGATTTGTGT 240

Db 356 GGTGCTGCTTGTGCTGCTTGTGCTGCTGCTGCTTGTGCTTCTGCGATTTGTGT 415

QY 241 ACTACTTGGGTTTGTGTTGAATTTATGATGACAGTTGCGTATTGT 283

Db 416 ACTACTTGGGTTTGTGTTGAATTTATGATGACAGTTGCGTATTGT 458

RESULT 15

ADX50588

ID ADX50588 standard; cDNA; 1216 BP.

XX AC ADX50588;

XX DT 21-APR-2005 (first entry)

XX DE Plant full length insert polynucleotide seqid 25328.

XX KW plant protectant; plant growth regulant; gene therapy; plant;

XX KW recombinant DNA construct; physical array; plant breeding marker;

XX KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

XX KW extreme osmotic condition; pathogen tolerance; pest tolerance;

XX KW growth rate; cell cycle pathway; disease resistance;

XX KW galactomannan production; lignin production; plant growth regulator;

XX KW yield; plant growth; plant development; seed oil; protein yield;

XX KW protein content; gene; ss.

XX OS Unidentified.

XX XX US2004034888-A1.

XX PD 19-FEB-2004.

XX PF 28-APR-2003; 2003US-00425114.

XX PR 06-MAY-1999; 99US-00304517.

XX PR 05-NOV-2001; 2001US-00985678.

XX PA (LIUJ/) LIU J.

PA	(ZHOU//)	ZHOU Y.
PA	(KOVA//)	KOVALIC D K.
PA	(SCRE//)	SCREEN S E.
PA	(TABA//)	TABASKA J E.
PA	(CAOY//)	CAO Y.

PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
DR WPI: 2004-180133/17.

PT New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for improving yield.

PS Claim 1: SEQ ID NO 25328: 15pp: English.

The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at <http://seqdata.uspto.gov/sequence.html?DocID:2004034988>. The polynucleotide of the invention is also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomanan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one or stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the invention.

SQ Sequence 1216 BP; 282 A; 342 C; 402 G; 190 T; 0 U; 0 Other;

Query Match	84.6%;	Score 278.4;	DB 13;	Length 1216;
Best Local Similarity	98.6%;	Pred. No. 4.4e-75;		
Matches 279;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	1	GGTCGACGCTGTCGGTGTCCGTACGTTCTGGCCGGCCGGGCGCTTGGCGCGCGATC	60	
Db	934	GGTCGACGCTGTCGGTGTCCGTACGTTCTGGCCGGCCGGGCGCTTGGCGCGCGATC	993	
Qy	61	AGAACCGTTCGGTTGGCGGTGTGCTGCTCTGGTTTCTTAAATTTTACCAAGTTCTGTT	120	
Db	994	AGAACCGTTCGGTTGGCGGTGTGCTGCTCTGGTTTCTTAAATTTTACCAAGTTCTGTT	1053	
Qy	121	CAAGGTGGATCGCGTGTCAAGGCCCGTGTCTTTAAANACCCACCGGCACTGGCAGTGA	180	
Db	1054	CAAGGTGGATCGCGTGTCAAGGTCCGTGTGCTTTAAAGACCCACCGGCACTGGCAGTGA	1113	
Qy	181	GTGTTGCTGCTTGTGTAGGCTTTTGGTACGTATGGGCTTTATTTGCTTCTCGATTTGTGT	240	
Db	1114	GTGTTGCTGCTTGTGTAGGCTTTTGGTACGTATGGGCTTTATTTGCTTCTCGATTTGTGT	1173	
Qy	241	ACTACTGGGTTTGTGAAATTATATGANCAGTTGCGTATTGT	283	
Db	1174	ACTACTGGGTTTGTGAAATTATATGAGCAGTTGCGTATTGT	1216	

Search completed: March 8, 2006, 04:18:51
Job time : 386.692 secs

181 GTGTTGCTGCTTGTGTAGGCTTTGGTACGTATGGGCTTTATTTCCTTCGGATGTTGTGT 240


```

KEYWORDS  FLI CDNA.
SOURCE      Zea mays
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 722)
AUTHORS     Lai, J., Dey, N., Kim C.-S., Bharti, A.K., Rudd, S., Mayer, K.F.X.,
            Larkins, B., Becraft, P. and Messing, J.
TITLE       Characterization of the maize endosperm transcriptome and its
            comparison to the rice genome
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 722)
AUTHORS     Lai, J., Dey, N., Kim C.-S., Bharti, A.K., Rudd, S., Mayer, K.F.X.,
            Larkins, B., Becraft, P. and Messing, J.
TITLE       Direct Submission
JOURNAL     Submitted (27-OCT-2004) Waksman Institute, Rutgers University, 190
            Frelinghuysen Rd, Piscataway, NJ 08854, USA
FEATURES   Location/Qualifiers
            source
            1..722
            /organism="Zea mays"
            /mol_type="mRNA"
            /db_xref="taxon:4577"
            /clone="Contig566.P"

ORIGIN
Query Match      89.2%; Score 293.4; DB 15; Length 722;
Best Local Similarity 98.7%; Pred. No. 3e-72;
Matches 294; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY  1  GGTCCAGCGTGTGGTGTCCGTACGTTCTGGCCGCCCGGCTTGGCGCGCGATC 60
DB  410 GGTCCAGCGTGTGGTGTCCGTACGTTCTGGCCGCCCGGCTTGGCGCGCGATC 469

QY  61  AGAAGCGTGTGGTGTGGTGTCTCTGCTTCTTAAATTTTACCAAGTTGTTT 120
DB  470 AGAAGCGTGTGGTGTGGTGTCTCTGCTTCTTAAATTTTACCAAGTTGTTT 529

QY  121 CAAGTGATGATCGGTGGTCAAGCGCGGTGTCTTTAAANACCACCGGCTGGCAGTGA 180
DB  530 CAAGTGATGATCGGTGGTCAAGCGCGGTGTCTTTAAAGACCCACCGGCTGGCAGTGA 589

QY  181 GTGTTGCTGTGTGTAGCTTTGTAGCTATGGCTTTATTTGCTTGGATGTGTGT 240
DB  590 GTGTTGCTGTGTGTAGCTTTGTAGCTATGGCTTTATTTGCTTGGATGTGTGT 649

QY  241 ACTACTGGGTTTGTGTAATTAATGANCAGTTCGTATTGTAATTCAGCTGGGCTA 298
DB  650 ACTACTGGGTTTGTGTAATTAATGANCAGTTCGTATTGTAATTCAGCTGGGCTA 707

RESULT 5
LOCUS      AR059010                      1333 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5837848.
ACCESSION  AR059010
VERSION     AR059010.1 GI:5984587
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 1333)
AUTHORS     Ely, S., Evans, I.J. Jeffrey, and Schuch, W. Walter.
TITLE       Root-specific promoter
JOURNAL     Patent: US 5837848-A 1 17-NOV-1998;
FEATURES   Location/Qualifiers
            source
            1..1333
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match      27.7%; Score 91; DB 6; Length 1333;
Best Local Similarity 64.7%; Pred. No. 9.5e-15;
Matches 211; Conservative 0; Mismatches 83; Indels 32; Gaps 4;

QY  22  GTGTGCTTCTGCTTGTCTTAAATTTTACC--AAGTTTGTTCGAAGTGGATCGCGTGTG 81
DB  995  GTGCGAGTCGCGAGCTGTCTTGGCCGTGGCGCGGATTTAGAAGCTAGCTAGCGTTGGCA 1054

QY  82  GTGTGCTTCTGCTTGTCTTAAATTTTACC--AAGTTTGTTCGAAGTGGATCGCGTGTG 139
DB  1055 GTGTGCTTCTGCTTGTCTTAAATTTTACC--AAGTTTGTTCGAAGTGGATCGCGTGTG 1114

QY  140 AAGGCCCGTGTGCTTTA-----AANACCACCGGCACCTGGCAGTGAGTGTGCTGTG 193
DB  1115 AAGTCCGTGTGCTCTATTAAGTGGATGGCGTGACTCTGGCAGTGAGTGTGCTGTG 1174

QY  194 TGTAGCTTTGTGTAGTATGGCTTTATTTGCTTCTGGA-----232
DB  1175 TGTAGAGCTGTGTAGTATGGCTTTATTTTGGTCCCAAGTCAAAAGTCACGTCGGTGT 1234

QY  233 TGTGTGTACTACTTGGCTTTGTTGAATTAATGANCAGTTCGCTATTAATTCAGT 292
DB  1235 GGATGTTGTGTACTTGGCTTTGTTGA--ATTATGAGCAGCTGCGTGTGTAATTCGGCT 1291

QY  293 GGGCTACCTGGACATTTGTTATGTAAT 318
DB  1292 GGGCTACCTGGATGCGGTTAATAAT 1317

RESULT 6
LOCUS      BD272350                      1333 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Root-specific promoter.
ACCESSION  BD272350
VERSION     BD272350.1 GI:33082118
KEYWORDS   Zea mays
SOURCE     Zea mays
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 1333)
AUTHORS     Ely, S., Evans, I.J. and Schuch, W.W.
TITLE       Root-specific promoter
JOURNAL     Patent: JP 2002537760-A 1 12-NOV-2002;
            ADVANTA TECHNOLOGY LTD
            OS Zea mays (maize)
            PN JP 2002537760-A/1
            PD 12-NOV-2002
            PP 16-NOV-1998 JP 2000582576
            PT SUSAN ELY, IAN JEFFREY EVANS, WOLFGANG WALTER SCHUCH PC
            C12N15/09,C12N5/10//A01H5/00,C12N15/00,C12N5/00 CC a, c, t, g,
            other or unknown
            CC a, c, t, g, other or unknown
            CC a, c, t, g, other or unknown
            FH Key Location/Qualifiers
            FT modified base (139)
            FT modified base (582)
            FT modified base (588).
FEATURES   Location/Qualifiers
            source
            1..1333
            /organism="Zea mays"
            /mol_type="genomic DNA"
            /db_xref="taxon:4577"

ORIGIN
Query Match      27.7%; Score 91; DB 6; Length 1333;
Best Local Similarity 64.7%; Pred. No. 9.5e-15;
Matches 211; Conservative 0; Mismatches 83; Indels 32; Gaps 4;

QY  22  GTGTGCTTCTGCTTGTCTTAAATTTTACC--AAGTTTGTTCGAAGTGGATCGCGTGTG 81
DB  995  GTGCGAGTCGCGAGCTGTCTTGGCCGTGGCGCGGATTTAGAAGCTAGCTAGCGTTGGCA 1054

QY  82  GTGTGCTTCTGCTTGTCTTAAATTTTACC--AAGTTTGTTCGAAGTGGATCGCGTGTG 139

```


ORIGIN

Query Match 23.3%; Score 76.6; DB 6; Length 291;
 Best Local Similarity 76.4%; Pred. No. 1.1e-10;
 Matches 146; Conservative 0; Mismatches 36; Indels 9; Gaps 4;

QY 38 GCGCGGCGCTTGGCGCGGATCAGAAAGTTGCGTTGGCGTGTGNGT--GCTTCGGTT 95
 |||||
 DB 69 GCGCGGCGCTTGGCGGATC-AGAAAGTACTAGCTGGTGGCAATGGTTCGGTTCTGGTT 127
 |||||
 QY 96 TCGTTTAATTTTACCAGTTTGTTCAGGTGATCGCGTGTGTCAGGCCCGTGTGCTTT 155
 |||||
 DB 128 TCGTT---TTACAAAGTTTGTTCAGGTGATCGCTGTCAAGTTCGGTGTGCTTT 184
 |||||
 QY 156 AAANACCCACCGC---ACTGCAGTGTGCTGCTTGTGTAGGCTTTCGTAGCTAT 212
 |||||
 DB 185 TTAAGTGTGATCGCGTACTGCGCAGTGTGCTGTCTTGTGTAGGACGTGTACGTAC 244
 |||||
 QY 213 GCGCTTTAATT 223
 |||||
 DB 245 GCGCTTTAATT 255
 |||||

RESULT 10

BV079994
 LOCUS sc1186_p5 Ky21 Zea mays Ky21 233 bp DNA linear STS 30-SEP-2003
 DEFINITION tagged site.

ACCESSION BV079994
 VERSION BV079994.1 GI:37051651
 KEYWORDS STS.

SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 233)
 McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
 MPZ-UCI Joint SNP Discovery
 Unpublished (2003)

COMMENT

Contact: Brandon S. Gaut
 Dept. Ecology and Evolutionary Biology
 U.C. Irvine
 321 Steinhaus Hall, Irvine, CA 92697-2525, USA
 Tel: (949) 824-2564
 Fax: (949) 824-2181
 Email: bgaut@uci.edu
 Primer A: ACCAAAGTTTGTTCAGGTGGA
 Primer B: TTTTGGCGAACCACCAAGC
 Protocol:
 PCR amplification of genomic DNA
 Template: 50 ng
 Primer: each 0.5 uM
 dNTPs: each 200 uM
 Taq Polymerase: RedTaq (Sigma)
 Total Vol: 10 ul
 Amplicon sequencing
 ABI protocol - using d-Rhodamine terminator cycle
 sequencing ready reaction with amplitaq DNA polymerase FS
 Sequence ran on ABI 3700 sequencer.

Buffer:

Genomic DNA amplification
 RedTaq (Sigma)
 Sequencing buffer
 d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 36 40 40 32 37 37 40 40 35 40 40 40 46
 40 42 42 42 42 42 28 28 37 37 50 50 52 39 44 43 60 59
 64 69 71 77 80 77 80 77 80 55 50 50 58 69 74 74 82 90 88 82 79
 77 77 74 72 73 64 59 57 57 64 75 73 80 80 84 90 90 90 90.

FEATURES

Location/Qualifiers

source

1. .233
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="Ky21"
 /db_xref="taxon:4577"
 /clone_lib="Zea mays Ky21"
 /dev_stage="seedling"
 /note="Organ: leaf; genomic DNA from inbred line"
 <1. .>233

STS
ORIGIN

Query Match 22.1%; Score 72.8; DB 10; Length 233;
 Best Local Similarity 67.1%; Pred. No. 1.3e-09;
 Matches 141; Conservative 0; Mismatches 49; Indels 20; Gaps 2;

QY 115 TTGTTTCAAGTGGATCGCTGTGTCAGGCCGCTGTGCTTTAAANACCCACCGC---AC 171
 |||||
 DB 1 TTGTTTCAAGTGGATCGCTGTGTCAGGCCGCTGTGCTTTTAAAGTGGATCGCTGAC 60
 |||||
 QY 172 TGGCAGTGTGCTGCTGCTGTGTAGGCTTTGGTACGTATGGGCTTTATTGCTTCTGG 231
 |||||
 DB 61 TGGCAGTGTGCTGCTGCTGTGTAGGACGTGTGTACGCGGTTTATTGTTGTTCCA 120
 |||||
 QY 232 ATGTTGTGTACTACTTGGGTTTG-----TTGAATTATTATGANCAGTT 274
 |||||
 DB 121 AGTCAAAAGTCACGCTCGCTCTGGATGTGTGTACTGGGTTTGTGAATTATGACAGCT 180
 |||||

QY 275 GCGTATTGTAATTTCAGCTGGGCTACCTCGGA 304
 |||||
 DB 181 GCGCGTTGTAATTTCGCTGGGCTACCTCGGA 210
 |||||

RESULT 11

BV106706
 LOCUS PZA01565 B73(2) Zea mays B73(2) 233 bp DNA linear STS 13-MAR-2004
 DEFINITION tagged site.

ACCESSION BV106706
 VERSION BV106706.1 GI:45422660
 KEYWORDS STS.

SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 233)
 McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
 MPZ-UCI Joint SNP Discovery
 Unpublished (2003)

COMMENT

Contact: Brandon S. Gaut
 Dept. Ecology and Evolutionary Biology
 U.C. Irvine
 321 Steinhaus Hall, Irvine, CA 92697-2525, USA
 Tel: (949) 824-2564
 Fax: (949) 824-2181
 Email: bgaut@uci.edu
 Primer A: ACCAAAGTTTGTTCAGGTGGA
 Primer B: TTTTGGCGAACCACCAAGC
 Protocol:
 PCR amplification of genomic DNA
 Template: 50 ng
 Primer: each 0.5 uM
 dNTPs: each 200 uM
 Taq Polymerase: RedTaq (Sigma)
 Total Vol: 10 ul
 Amplicon sequencing
 ABI protocol - using d-Rhodamine terminator cycle
 sequencing ready reaction with amplitaq DNA polymerase FS
 Sequence ran on ABI 3700 sequencer.

Protocol:

PCR amplification of genomic DNA
 Template: 50 ng
 Primer: each 0.5 uM
 dNTPs: each 200 uM
 Taq Polymerase: RedTaq (Sigma)
 Total Vol: 10 ul

Amplicon sequencing

ABI protocol - using d-Rhodamine terminator cycle
 sequencing ready reaction with amplitaq DNA polymerase FS
 Sequence ran on ABI 3700 sequencer.

Buffer:

Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 40 40 48 34 37 40 40 40 37 42 42 51 56
56 56 56 47 42 42 43 37 37 40 40 40 40 37 40 35 30 42 42
43 56 56 88 90 70 66 66 55 55 66 78 77 74 76 84 90 90 86
86 80 74 69 71 60 60 57 57 69 76 78 81 90 90 90 90 90 90
84 84 85 45 45 28 28 28 42 40 45 87 89 82 74 77 77 77 77 73
77 79 90 90 81 81 81 81 77 90 86 85 74 74 82 79 75 77 80 80
82 90 85 72 72 72 72 72 75 88 88 90 80 80 80 85 85 90
90 90 83 89 78 83 84 79 79 85 85 90 89 89 83 86 82 82 82
83 90 80 89 80 82 69 71 81 78 84 84 84 77 77 71 73 73 83
83 88 90 80 78 74 76 76 76 77 65 57 55 60 57 61 54 71 69 40 40
40 56 22 22 22 22 56 47 47 42 42 42 56 47 56 40 46 44 40 40 48

FEATURES

Location/Qualifiers
1..233
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73(2)"
/db_xref="taxon:4577"
/clone_lib="Zea mays B73(2)"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1..>233

STS

ORIGIN
Query Match 22.1%; Score 72.8; DB 10; Length 233;
Best Local Similarity 67.1%; Pred. No. 1.3e-09;
Matches 141; Conservative 0; Mismatches 49; Indels 20; Gaps 2;

QY 115 TTGTTTCAAGTGGATCGGTCGAGCCGCTGTGCTTTAAANACCACCGGC---AC 171
Db 1 TTGTTTCAAGTGGATCGGTCGAGCCGCTGTGCTTTAAAGTGGATCGGTCGAC 60
QY 172 TGGCAGTCAGTGTCTGCTGTGTAGCTTTGGTACGTATGGGCTTTATTGCTTCTGG 231
Db 61 TGGCAGTCAGTGTCTGCTGTGTAGCTTTGGTACGTATGGGCTTTATTGCTTCTCA 120
QY 232 ATGTTGTGTACTACTTGGGTTTG-----TTGAATTATTATGANCAGTT 274
Db 121 AGTCAAAAGTCACGGTCGGTCGGATGTGTGTACTGCGTTTGTGAATTATGACAGCT 180
QY 275 GCGTATTGTAATCAGCTGGGCTACCTGGA 304
Db 181 GCGCGTTGTAATTCGGCTGGGCTACCTGGA 210

RESULT 12

BV106711
LOCUS PZA01565 Ky21 Zea mays Ky21 Zea mays STS 13-MAR-2004
DEFINITION 233 bp DNA linear STS genomic, sequence tagged site.

ACCESSION BV106711

VERSION BV106711.1 GI:45422666

KEYWORDS STS.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 233)

McMullen, M.D., Vroh Bi, I., Schroeder, S.S. and Gaut, B.S.

TITLE MPZ-UCI Joint SNP Discovery

JOURNAL Unpublished (2003)

COMMENT

Contact: Brandon S. Gaut

Dept. Ecology and Evolutionary Biology

U.C. Irvine

321 Steinhaus Hall, Irvine, CA 92697-2525, USA

Tel: (949) 824-2564

Fax: (949) 824-2181

Email: bgaut@uci.edu
Primer A: ACCAAAAGTTTGTTCACAGTGGA
Primer B: TTTTGGGAGAAACCAAGC
STS size: 233

Protocol:

PCR amplification of genomic DNA

Template: 50 ng

Primer: each 0.5 uM

dNTPs: each 200 uM

Taq Polymerase: RedTaq (Sigma)

Total Vol: 10 ul

Amplicon sequencing

ABI protocol - using d-Rhodamine terminator cycle

sequencing ready reaction with amplitaq DNA polymerase FS

Sequence ran on ABI 3700 sequencer.

Buffer:

Genomic DNA amplification

RedTaq (Sigma)

Sequencing buffer

d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 36 40 40 32 37 40 40 35 40 40 40 46
40 42 42 42 42 42 28 28 37 37 37 50 50 50 52 39 44 43 60 59
64 69 71 77 80 77 60 55 55 50 58 69 74 69 74 74 82 90 88 82 79
77 77 74 72 73 64 59 57 64 75 73 80 80 84 90 90 90 90 90 90
77 80 80 82 81 76 57 60 52 86 81 77 77 78 73 72 72 72 72 72 72
75 85 86 90 90 81 82 78 77 77 90 86 85 74 74 82 85 76 80 84 84
84 90 90 77 70 70 70 72 80 80 90 90 90 90 90 82 82 77 77 77 90
84 86 90 80 88 86 78 75 80 80 75 80 90 90 88 90 83 86 82 82 82
86 90 90 86 90 70 70 74 79 78 80 82 80 74 76 73 72 71 84 85 87
87 85 90 85 90 90 78 81 77 90 78 66 58 57 61 57 56 74 74 45 45
45 56 24 24 24 24 56 56 47 42 42 56 56 56 40 40 46 40 40 37 40

FEATURES

Location/Qualifiers

1..233

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="Ky21"

/db_xref="taxon:4577"

/clone_lib="Zea mays Ky21"

/dev_stage="seedling"

/note="Organ: leaf; genomic DNA from inbred line"

<1..>233

STS

ORIGIN

Query Match 22.1%; Score 72.8; DB 10; Length 233;
Best Local Similarity 67.1%; Pred. No. 1.3e-09;
Matches 141; Conservative 0; Mismatches 49; Indels 20; Gaps 2;

QY 115 TTGTTTCAAGTGGATCGGTCGAGCCGCTGTGCTTTAAANACCACCGGC---AC 171
Db 1 TTGTTTCAAGTGGATCGGTCGAGCCGCTGTGCTTTAAAGTGGATCGGTCGAC 60
QY 172 TGGCAGTCAGTGTCTGCTGTGTAGCTTTGGTACGTATGGGCTTTATTGCTTCTGG 231
Db 61 TGGCAGTCAGTGTCTGCTGTGTAGCTTTGGTACGTATGGGCTTTATTGCTTCTCA 120
QY 232 ATGTTGTGTACTACTTGGGTTTG-----TTGAATTATTATGANCAGTT 274
Db 121 AGTCAAAAGTCACGGTCGGTCGGATGTGTGTACTGCGTTTGTGAATTATGACAGCT 180
QY 275 GCGTATTGTAATCAGCTGGGCTACCTGGA 304
Db 181 GCGCGTTGTAATTCGGCTGGGCTACCTGGA 210

RESULT 13

BV079992

LOCUS

DEFINITION

tagged site.

ACCESSION BV079992

VERSION BV079992.1 GI:37051649

237 bp DNA linear STS 30-SEP-2003
sc1186.p5 I114H Zea mays I114H Zea mays STS genomic, sequence
tagged site.
BV079992
BV079992.1 GI:37051649

Best Local Similarity 68.3%; Pred. No. 1.7e-09;
Matches 157; Conservative 0; Mismatches 43; Indels 30; Gaps 3;
QY 116 TGTTCACAGGTGATCGCGTGTCAAGCCCGGTGCTTTAAANAC-----CCACCGGC 169
Db 1 TGTTCACAGGTGATCGCGTGTCAAGTCCGTGTCTATTAAAGTGGATCGGTGAC 60
QY 170 ACTGCAGTGAGTGTCTGCTTGTGTAGGCTTGGTACGTATGGCTTTATTTCCTTCT 229
Db 61 TCTGCAGTGAGTGTCTGCTTGTGTAGGACGTGTACGTACGGGCTTTATTTCGTCC 120
QY 230 GGA-----TGTTGTGTACTTGGTGTGGTGTGGTAAATTATTATGA 268
Db 121 CAAAGTCAAAAGTCACGGTCGGTCTCGATGTGTGTACTTGGTGTGGTAAATTATTATGA 177
QY 269 NCAGTGTGCTATTGTAATTCAGCTGGGCTACCTGGACATTGTAATGTAAT 318
Db 178 GCAGCTGCGTGTGTAATTCGGCTCGGCTACCTGGATCGGTAAATAATT 227

RESULT 15
BV079989
LOCUS sc1186_p5 B73 Zea mays B73 Zea mays STS 30-SEP-2003
DEFINITION linear STS genomic, sequence tagged
ACCESSION BV079989
VERSION BV079989.1 GI:37051646
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 232)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
Unpublished (2003)

Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ACCAAAGTTTGTTCAGGTGGA
Primer B: TTTTGGGAGAAACCAAGC
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with AmpliTaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 37 31 31 33 35 35 37 56 56 56 46 42
56 56 56 43 44 38 35 35 35 27 27 27 37 37 35 50 44 56 61 62 71
83 85 88 83 71 66 66 55 55 56 78 78 72 74 84 90 85 90 85 80 80
74 74 69 63 60 61 62 65 78 85 90 90 90 90 90 90 90 90 90.

FEATURES
source
1..232
/organism="Zea mays"
/mol_type="genomic DNA"

/cultivar="B73"
/db_xref="taxon:4577"
/clone_lib="Zea mays B73"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1..>232
STS
ORIGIN
Query Match 21.5%; Score 70.8; DB 10; Length 232;
Best Local Similarity 66.8%; Pred. No. 4.8e-09;
Matches 139; Conservative 0; Mismatches 49; Indels 20; Gaps 2;
QY 117 GTTTCACAGGTGATCGCGTGTCAAGCCCGGTGCTTTAAANACCCAC---CGGCACTG 173
Db 1 GTTTCACAGGTGATCGCGTGTCAAGTCCGTGTCTTTTAAAGTGGATCGGTGACTG 60
QY 174 GCAGTGAGTGTGCTGCTTGTGTAGGCTTTGGTACGTATGGGCTTTATTTCCTTCTGGAT 233
Db 61 GCAGTGAGTGTGCTGCTTGTGTAGGACGTGTACGGGTTTATTTCCTTCCAAG 120
QY 234 GTTGTGTACTACTTGGGTTTG-----TTGAATTATTATGANCAGTTGC 276
Db 121 TCAAAAGTTCACGGTCCGTCTGGATGTTGTGTACTGGGTTTGTGAATTATGAGCAGCTGC 180
QY 277 GTATTGTAATTCAGCTGGGCTACCTGGA 304
Db 181 GCGTTGTAATTCGGCTGGGCTACCTGGA 208

Search completed: March 8, 2006, 06:32:08
Job time : 2384.09 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model
Run on: March 8, 2006, 04:07:00 ; Search time 2667.19 Seconds
(without alignments)
5823.847 Million cell updates/sec

Title: US-10-603-524A-1
Perfect score: 329
Sequence: 1 ggtcgacggtgctgctgc.....tgtattataaatgctttgc 332

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_hic:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_est7:
9: gb_gss1:
10: gb_gss2:
11: gb_gss3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	327.4	99.5	519	3	BM382021
C 2	327.4	99.5	559	3	BM381414
C 3	327.4	99.5	615	1	AI649488
C 4	327.4	99.5	615	8	DN204249
C 5	327.4	99.5	660	6	CF629927
C 6	327.4	99.5	675	8	DN212434
C 7	327.4	99.5	753	8	DR955206
C 8	327.4	99.5	782	9	CT700159
C 9	325.8	99.0	444	7	CN844293
C 10	325.8	99.0	603	7	CN827377
C 11	324.2	98.5	412	6	CF633415
C 12	321.8	97.8	443	7	CN844286
C 13	319.4	97.1	434	2	BG841223
C 14	313.4	95.3	629	6	CF625618
C 15	311.6	94.7	449	6	CB380509
C 16	311.2	94.6	687	8	DN232860
C 17	303.4	92.2	618	8	DN232769
C 18	286.4	87.1	330	6	DN828411
C 19	283.4	85.1	490	6	CF626006
C 20	283.4	86.1	568	6	CF628060
C 21	279.6	85.0	634	1	AI629748
C 22	278.4	84.6	524	6	CF629847

C 23	278.4	84.6	665	6	CF625636
C 24	278.4	84.6	745	7	CK985786
C 25	278.4	84.6	1256	4	AY111114
C 26	278.4	84.5	605	8	DN221053
C 27	275.6	83.8	461	8	DN210598
C 28	274.4	83.4	294	6	CB381621
C 29	274.4	83.4	518	1	AI586566
C 30	270.6	82.2	521	3	BM379174
C 31	270.4	82.2	637	6	CD001819
C 32	270.2	82.1	794	9	CC700174
C 33	266.4	81.0	549	6	CD484944
C 34	264.4	80.4	594	6	CD573321
C 35	258.4	78.5	305	7	CV071480
C 36	253.8	77.1	588	3	BM382407
C 37	241	73.3	266	6	CB351546
C 38	237.8	72.3	273	7	CN845511
C 39	237.4	72.2	559	3	BM337639
C 40	237.4	72.2	586	3	BM379625
C 41	232.6	70.7	434	6	CF057128
C 42	232.6	70.7	491	5	BQ486909
C 43	231	70.2	432	6	CF057584
C 44	223.4	67.9	696	3	BM334944
C 45	221.6	67.4	611	3	BM339531

ALIGNMENTS

RESULT 1
BM382021/c
LOCUS BM382021 519 bp mRNA linear EST 16-JAN-2002
DEFINITION MEST543-E03.univ ISUM6 Zea mays cdna clone MEST543-E03 3', mRNA
ACCESSION BM382021
VERSION BM382021.1 GI:18180811
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 519)
Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S.
AUTHORS Expressed Sequence Tags from B73 Maize: various stages and tissues
TITLE including seedlings treated with a variety of hormones
JOURNAL Unpublished (2001)
COMMENT Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
Tel: 515-294-0975
Fax: 515-294-5256
Email: schnable@iastate.edu
Individual basecall and confidence value were assigned using the
Phred software(<http://www.phrap.org/>). Overall sequence quality
assessment and vector trimming was conducted using the Lucy
software (version 1.16s, <http://www.tigr.org/softlab/>). Lucy
parameters were set to ensure an overall trimmed quality of 97.5%
or better without any vector fragments in the chosen high quality
region of each sequence. Low-quality bases between the poly-T and
the high-quality region were replaced with N's to serve as spacers
using a Perl program (est_process.pl), written by Dr. Hui-Hsien
Chou.
PCR Primers
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer Sp6 (ATT TAG GTG ACA CTA TAG)
Seq primer: universal (GTA AAA CGA CGG CCA GT)
POLYA-Yes.
Location/Qualifiers
1..519
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"

33

Email: walbot@stanford.edu

Query Match 99.5%; Score 327.4; DB 1; Length 615;

Matches 328; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
1 GGTCCACGGTGTGGGTGTCGTGCTAGCTTCTGGCGCGCGCGCCTTGGCGCGCGCATC 60

Qy 1 GGTGGAGCGTGTGGTGTCCGTCGTACGTTCTGGCCCGGCCGCGCGATC 60
|||||
348 GGTTCGAGCGTGTGGTGTCCGTCGTACGTTCTGGCCCGGCCGCGCGATC 288
Db

QY 61 AGAANCGTTGCGTTGCGGTGTGTGCTTCTGCTTAATTTACCAAGTTTGT 120

100

DD 288 AGAAGCGIIGCGITGGCGIGIGIGIGCTCTGGTITGCTTTAAATTTACCAAGTTTGTIT 229

QY 121 CAAGGTGGATCGCGTGGTCAAGCCCGTGTGCTTTAAANACCCACCGCACTGGCAGTGA 180

228 C A G G T G G A T C G C G T G C T C A A G C T C C G T C T C G T T T A A A C A C C C A C C C C A C T C A 168

QUESTION

181 GTGTTGCTGCTTGTGTAGGCTTTGGTACGTATGGGCTTTATTTGCTTCTGGATGTTGTGT 240

db 168 GTGTTGCTGCTTGTGTA GCGTTTGGTACGTA TGGGCTTTATTTGCTTCTGGATGTTGTGT 109

Downloaded from <http://ajph.org/> on November 10, 2014

241 ACTACTTGGGTTTGTGTAATTAATGANCAGTTGCGTATTGTAATTCAGCTGGCTACC 300
QY

Db 108 ACTACTTGGGTTGTTGAATTATATGAGCAGTTGCGTATTGTAATTCAGCTGGGCTACC 49

THE

QY 301 TGGACATGTATAGTATTAATAAATGCTTTC 332

Db . 48 TGGACATTGTTATGTATTAAATAAATGCTTTGC 17

RESULT 4

DN204249/c

LOCUS	DN204249	615 bp	mRNA	linear	EST 28-FEB-2000
DEFINITION	MEST801 E08 T7-1	UCA-ZMSM-YZ3	zms	cdna	cdna

ACCESSION DN204249

VERSION DN204249.1 GI:60337276

KEYWORDS EST. Zea mays
SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

epimatophyta; magnoliophyta; lillopsiua; foaceae; foates; foaceae; foaccad
clade; panicoideae; andropogoneae; Zea.

REFERENCE 1 (bases 1 to 615)

AUTHORS
Chen, H.D., Zhang, X., Zhou, R.L., Arias L, A.C., Shendelman, J.M.,
Zazubovits, N., Borsuk, L.A., Emrich, S.J., Ashlock, D.A., Scanlon, M.J.

and Schnable, P.S.

TITLE Expressed Sequence Tags from B73 Maize Shoot Apical Meristems
JOURNAL Unpublished (2004)

DOCUMENT : UNPUBLISHED (2004)
COMMENT
Contact: Patrick S. Schnable

Schnable Laboratory

Iowa State University
2035B R. J. Carver Co-Lab Ames IA 50011-3650 USA

Tel: 515-294-0975

Fax: 515-294-5256

FEATURES

Location/Qualifiers

Email: schmable@iastate.edu.

source	1. .615
--------	---------

```
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="inbred B73"
/db_xref="taxon:4577"
/tissue_type="Vegetative Shoot Apical Meristem (SAM) and
leaf primordia staged P1-P4"
/lab_host="XLI-Blue"
/clone_lib="UGA-ZmSAM-X22"
/note="Organ: Shoot apex, Vector: Uni-Zap XR, Site 1:
EcoRI; Site 2: XhoI; This library was constructed by
Xiaolan Zhang. Vegetative Shoot Apical Meristem (SAM) and
leaf primordia staged P1-P4 from 14-17 day-after
germination seedlings were quickly dissected into dry ice
under a light microscope. Total RNA was isolated using
Trizol and mRNA was purified with Dynal Oligo-DT25.
ds-cDNA molecules were generated as follows. First-strand
cDNA was prepared from oligo-dT selected mRNA by priming
with an XhoI oligo-dT primer
(5'-CAGAGAGAGAGAGAGAGACTAGTCTCGAGTGTTCCTTTTTCCTTTT).
The resulting DNA:RNA hybrid was treated with RNase H and
used as a template for DNA PolI-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with XhoI and size-selected to be
>600 bp. The resulting molecules were directionally cloned
into the EcoRI and XhoI sites of the Uni-Zap XR vector.
The lambda library was packaged with Gigapack III Gold
packaging extract and was mass excised by XLI-Blue cells
and ExAestit helper phage. Excised phagemids were titred
in SOLR cells and plated onto LB-ampicillin agar plates.
Base calling was conducted using Phred. Trimming was
performed using Lucy with the following criteria:
1-minium 200 -error 0.01 0.01 -bracket 10 0.01). A low
complexity filter was applied and additional trimming was
conducted to remove E. coli, vector, and organelle
contamination. After processing ~30% of the sequences
contained a minimum of 10 Ts at the beginning of the
sequence. For reasons that are not understood many of the
clones in this library lack an XhoI site at their 3'
ends."
```

ORIGIN

```
Query Match 99.5%; Score 327.4; DB 8; Length 615;
Best Local Similarity 98.8%; Pred. No. 6.7e-82;
Matches 328; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGTCCAGCGTGTGCGTTCGTCTGATGTTCTGCGCGCGCGCGCTTGGCGCGCGATC 60
Db 332 GGTCCAGCGTGTGCGTTCGTCTGATGTTCTGCGCGCGCGCGCTTGGCGCGCGATC 273
QY 61 AGAANCCTGCTGCGCGTGTGCGTTCGTCTGATGTTCTTAAATTTTACCAGTTGTTT 120
Dd 272 AGAAGCTGCTGCGCGTGTGCGTTCGTCTGATGTTCTTAAATTTTACCAGTTGTTT 213
QY 121 CAAGGTGGATCGCGTGTGCAAGCGCGCGTGTCTTTAAANACCCAGCGCACTGGCAGTGA 180
Dd 212 CAAGGTGGATCGCGTGTGCAAGTTCGTGTGCTTTAAAGACCCAGCGCACTGGCAGTGA 153
QY 181 GGTGTTGCTGCTGTGTAGCGTTTGTGTAGCTATGCGGCTTTATTTGCTTCTGAGTTGTGT 240
Dd 152 GTGTGCTGCTGTGTAGCGTTTGTGTAGCTATGCGGCTTTATTTGCTTCTGATGTTGTGT 93
QY 241 ACTACTCGGTTTGTGTAATTTATTTGATGAGTTCGATGTTGTAATTCAGCTGGCGTACC 300
Dd 92 ACTACTCGGTTTGTGTAATTTATTTGAGCAGTTCGATGTTGTAATTCAGCTGGCGTACC 33
QY 301 TCGACATGTTATGTAATTAATAAATGCTTTTC 332
Dd 32 TGGACATGTTATGTAATTAATAAATGCTTTTC 1
```

```
RESULT 5
CF629927/c
LOCUS CF629927 660 bp mRNA linear EST 02-OCT-2003
```

DEFINITION zmrws48 OA20-006-h12.s3 zmrws48 Zea mays cDNA 3', mRNA sequence.
ACCESSION CF629927
VERSION CF629927.1 GI:37385560
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE 1 (bases 1 to 660)
AUTHORS Bohnert, H., Sharp, R.E., Springer, G.K., Poroyko, V., Fredrickson, M.,
Sharp, L.G., Spollen, W.G., Ries, J., Guillen, A., Khambati, A.,
Topinka, C., Davis, G.E., Schachtman, D., Wu, Y., and Nguyen, H.T.
NSF Grant DBI-0211842: Functional Genomics of Root Growth and Root
Signaling Under Drought
Unpublished (2003)

JOURNAL
COMMENT Contact: Hans Bohnert
University of Illinois, Urbana-Champaign
1201 West Gregory Drive, Urbana, IL 61801, USA
Tel: 217-265-5475
Fax: 217-333-5574
Email: bohnert@life.uiuc.edu
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1..660
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
/clone_lib="zmrws48"

/note="Samples were collected in Robert E. Sharp's lab (University of Missouri-Columbia) to construct three normalized cDNA libraries. Dark-grown maize seedlings with primary roots 12-20 mm in length were transplanted to high and harvested at 5 h and 48 h after transplanting. About 1,000 roots were used for each of the low water potential libraries (zmrws05 and zmrws48) while 500 roots were combined from each of the two time points at high water potential (zmrw00). Each root was divided into 4 segments (distances are from the junction of the root apex and root cap): segment 1, 0-3 mm plus the root cap; segment 2, 3-7 mm; segment 3, 7-12 mm; segment 4, 12-20 mm. (For details of conditions see (1) with nutrient modifications as in (2)). The three normalized cDNA libraries were constructed in the lab of Hans Bohnert (University of Illinois-UC). Total RNA was extracted by the 'hot phenol' method (Plant Molecular Biology manual, D5: 1-13, 2nd ed., 1997). This method worked in eliminating carbohydrate material present in the root tips. The integrity of the RNA was verified by denaturing agarose gels and spectrophotometry (ratio A260/280). Poly(A)+mRNA was isolated twice from total RNA using the Oligotex Direct mRNA kit (Qiagen). Poly(A)+ mRNA was converted to double-stranded cDNA and tagged by using modified Oligo(dT) primers. One of 4 sequence tags corresponding to a different segment of the root was added to the 3'-end of the modified Oligo(dT) primers, including a NotI site and used to reverse transcribe the segment-specific mRNAs into cDNAs. Each library contains all four tags. A suffix (s1, s2, s3, or s4) has been added to each sequence identifier to designate which region of the root (root segment 1, 2, 3, or 4) the sequence was found in based on the identification of the tag. A suffix of s0 indicates that the sequence tag, and hence the source segment, could not be identified. The double stranded cDNAs were size-selected (>450 bp). Size selected cDNAs were adapted with EcoRI adaptors at both ends, and then digested with NotI. The cDNA was directionally cloned into EcoRI-NotI digested pBS II SK(+) phagemid vector (Stratagene) and electroporated into E.coli DH10B. The total number of white colony forming units (cfu) in the primary libraries before amplification was as follows: zmrws05: 3.37 x 106; zmrws48: 4.87 x 106; zmrw00: 3 x 106. The background of empty clones was less than 1%.


```

|||||
118 ACTACTTGGGTTTGTAATTATAGCAGCTGCCTATTGTAAATTCAGCTGGCGTACC 59
|||||
301 TGGACATTTGATGATTATAAATGCTTTGC 332
|||||
58 TGGACATTTGATGATTATAAATGCTTTGC 27
|||||

DR955206          753 bp      mRNA       linear     EST 03-AUG-2005
ZM_BF50049D21.f ZM_BFB Zea mays cDNA 3', mRNA sequence.
DR955206
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 753)
Kim H., Collura K., Wisotski M., Smart D., Kudrna D., Muller C.,
Rao K., Hallett K., Wing R., Soderlund C., Walbot V. and Yu Y.
Maize Full-length cDNA Project
Unpublished (2005)
Contact: Yeisoo Yu
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9585
Fax: 520 621 1259
Email: yeisoo@genome.arizona.edu
Plate: 0049 row: D column: 21.
Location/Qualifiers
1. .753
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="mixed (silks, husks, ears, pollen, shoot
tips, leaf, root tips, whole seed, embryo)"
/dev_stage="varies by tissue"
/lab_host="PH10B T1 phage resistant"
/clone_lib="ZM BFB"
/notes="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:
NotI; Maize Full length cDNA library (3530 library)
created by Invitrogen from multiple tissues; Organ: silks,
husks, ears, pollen, shoot tips, leaf, root tips, whole
seed, embryo. This is a Gateway compatible vector,
permitting clone movement to new vector backbones for
expression in diverse host cells using recombination
rather than restriction enzymes. poly(A)+ mRNA was
prepared by Invitrogen, and equimolar amounts of RNA from
each of the 12 tissue samples were mixed together for
selection of mRNA with a 5' cap. After synthesis of cDNA,
a normalization step was conducted against the mixture of
RNA sources. Tissues prepared: 1. just emerging silks; 2.
inner husks from ears of sample #1; 3. 20 dap aleurone; 4.
immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to
2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from
15 day old seedlings; all leaves with an expanded or
partially expanded sheath were removed; 8. mature leaf
tissue; 9. 0.5 cm long root tips from 15 day old
seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and
embryo; 12. 17 dap endosperm and embryo. All of the
sequenced clones in Maize Full-length cDNA Project will be
archived at the University of Arizona. Clones, high
density filters and amplified library can be ordered from
the University of Arizona
(http://www.genome.arizona.edu/orders/)."

FEATURES
source
Query Match          99.5%; Score 327.4; DB 8; Length 753;
Best Local Similarity 98.8%; Pred. NO. 6.9e-82; Indels 0; Gaps 0
Matches 328; Conservative 0; Mismatches 4;

ORIGIN
Query Match          99.5%; Score 327.4; DB 9; Length 782;
Best Local Similarity 98.8%; Pred. NO. 7e-82; Indels 0; Gaps 0
Matches 328; Conservative 0; Mismatches 4;

RESULTS
RESULT 8
CC700159/c
LOCUS
DEFINITION
CC700159 genomic survey sequence.
ACCESSION
VERSION CC700159.1 GI:32104935
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 782)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Reinick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSES: OGUE101TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: methylation filtered.
Location/Qualifiers
1. .782
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0421A01"
/clone_lib="ZM_0.7_1.5_KB"
/notes="Vector: pBCSK; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match          99.5%; Score 327.4; DB 9; Length 782;
Best Local Similarity 98.8%; Pred. NO. 7e-82; Indels 0; Gaps 0
Matches 328; Conservative 0; Mismatches 4;

RESULTS
RESULT 9
CC700159/c
LOCUS
DEFINITION
CC700159 genomic survey sequence.
ACCESSION
VERSION CC700159.1 GI:32104935
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 782)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Reinick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSES: OGUE101TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: methylation filtered.
Location/Qualifiers
1. .782
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0421A01"
/clone_lib="ZM_0.7_1.5_KB"
/notes="Vector: pBCSK; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

```



```

Db      557  GGTTCGACGGTGTGCGTGTCCGTCGACGTTCTGGCCGCGCCCTTGGCGCGCGATC 498
QY      61   AGAAGCGTTGCGTGTGCGTGTGCGTCTTCTGCTTTTAAATTTTACCAAGTTTGT 120
Db      497  AGAAGCGTTGCGTGTGCGTGTGCGTCTTCTGCTTTTAAATTTTACCAAGTTTGT 438
QY      121  CAAGGTGGATCGCGTGTCAAGCCCGTGTCTTTAAANACCCACCGGCACCTGGCAGTGA 180
Db      437  CAAGGTGGATCGCGTGTCAAGCCCGTGTCTTTAAAGACCCACCGGCACCTGGCAGTGA 378
QY      181  GTGTTGCTGCTGTGTGAGGCTTTGTACGATGAGGCTTTATTTGCTTCTGGAATGTTGT 240
Db      377  GTGTTGCTGCTGTGTGAGGCTTTGTACGATGAGGCTTTATTTGCTTCTGGAATGTTGT 318
QY      241  ACTACTTGGGTTTGTGTAATTATGANCAGTTGCGTATTGTAATTCACTGGGCTACC 300
Db      317  ACTACTTGGGTTTGTGTAATTATGAGCAGTTGCGTATTGTAATTCACTGGGCTACC 258
QY      301  TGGACATTTGTTATGTAATTAAATGCTTTGC 332
Db      257  TGGACATTTGTTATGTAATTAAATGCTTTGC 226

```

```

RESULT 9
CN844293
LOCUS   EST2243 Zea mays embryo sac cDNA library Zea mays cDNA clone ES5257
DEFINITION
ACCESSION CN844293
VERSION   CN844293.1 GI:47961584
KEYWORDS EST.
SOURCE   Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS Yang, H. and McCormick, S.
TITLE   "Transcriptome of Zea mays embryo sac
JOURNAL Unpublished (2004)
COMMENT Contact: Yang, H.; McCormick, S.
Plant Gene Expression Center
USDA/ARS
800 Buchanan St. Albany, CA 94710, USA
Tel: 510 559 5906
Fax: 510 559 5678
Email: shellam@nature.berkeley.edu.

```

```

FEATURES
source
1..444
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="Al88"
/db_xref="taxon:4577"
/clone="ES5257"
/cell_type="embryo sac"
/clone_lib="Zea mays embryo sac cDNA library"
/notes="Vector: Clontech Triplex2; Embryo sacs were isolated with enzymatic maceration and manual microdissection. RNA was extracted from the embryo sacs. A cDNA library was constructed by oligo dt priming using the Clontech SMART cDNA synthesis kit. The cDNAs were directionally cloned."

```

```

ORIGIN
Query Match 99.0%; Score 325.8; DB 7; Length 444;
Best Local Similarity 98.5%; Pred. No. 1.8e-81;
Matches 327; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

```

QY      1   GGTCCAGCGTGTGCGTGTCCGTCGACGTTCTGGCCGCGCCCTTGGCGCGCGATC 60
Db      76  GGTCCAGCGTGTGCGTGTCCGTCGACGTTCTGGCCGCGCCCTTGGCGCGCGATC 135

```

```

QY      61   AGAAGCGTTGCGTGTGCGTGTGCGTCTTCTGCTTTTAAATTTTACCAAGTTTGT 120
Db      136  AGAAGCGTTGCGTGTGCGTGTGCGTCTTCTGCTTTTAAATTTTACCAAGTTTGT 195
QY      121  CAAGGTGGATCGCGTGTCAAGCCCGTGTCTTTAAANACCCACCGGCACCTGGCAGTGA 180
Db      196  CAAGGTGGATCGCGTGTCAAGCCCGTGTCTTTAAAGACCCACCGGCACCTGGCAGTGA 255
QY      181  GTGTTGCTGCTGTGTGAGGCTTTGTACGATGAGGCTTTATTTGCTTCTGGAATGTTGT 240
Db      256  GTGTTGCTGCTGTGTGAGGCTTTGTACGATGAGGCTTTATTTGCTTCTGGAATGTTGT 315
QY      241  ACTACTTGGGTTTGTGTAATTATGANCAGTTGCGTATTGTAATTCACTGGGCTACC 300
Db      316  ACTACTTGGGTTTGTGTAATTATGAGCAGTTGCGTATTGTAATTCACTGGGCTACC 375
QY      301  TGGACATTTGTTATGTAATTAAATGCTTTGC 332
Db      376  TGGACATTTGTTATGTAATTAAATGCTTTGC 407

```

```

RESULT 10
CN827377/c
LOCUS   CK827377
DEFINITION zmrsub1_0B20-006-a09.s0 zmrsub1 Zea mays cDNA 3', mRNA sequence.
ACCESSION CK827377
VERSION   CK827377.1 GI:44900832
KEYWORDS EST.
SOURCE   Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS Bohnert, H., Sharp, R.E., Springer, G.K., Poroyko, V., Fredrickson, M.,
Sharp, D.G., Spollen, W.G., Ries, J., Guillen, A., Khambati, A.,
Topinka, C., Davis, G.E., Schachtman, D., Wu, Y., and Nguyen, H.T.
TITLE   NSF Grant DBI-0211842: Functional Genomics of Root Growth and Root
JOURNAL Signaling Under Drought
COMMENT Unpublished (2003)
Contact: Hans Bohnert
University of Illinois, Urbana-Champaign
1201 West Gregory Drive, Urbana, IL 61801, USA
Tel: 217-265-5475
Fax: 217-333-5574
Email: bohnert@life.uiuc.edu
POLYA=Yes.

```

```

FEATURES
source
1..603
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
/clone_lib="zmrsub1"
/notes="(1) The zmrsub1 library was created by subtracting the well-watered maize root libraries zmrws05 and zmrws48. The 3 starting libraries are described below in (3). (2) Purified plasmid preps from zmrws05 and zmrws48 were combined. Sequenced clones from the zmrws05 library were pooled and converted into single-stranded circles and used as a driver for subtraction. The PCR products from the driver were hybridized with the single-stranded version of the zmrws05-zmrws48 library for 88 hours at 30 oC. Unhybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DH10B cells to generate the subtracted library. The total number of clones was 2 x 106 cfu. Background of empty clones (detected by blue/white selection on agar plates) was approximately 10%. Insert size of the subtracted library, determined by PCR of the entire library, ranges from 0.5 to 2.1kb). (3) Root samples were collected in Robert E. Sharp's lab (University of Missouri-Columbia) to construct three

```


(2)). The three normalized cDNA libraries were constructed in the lab of Hans Bohnert (University of Illinois-UC). Total RNA was extracted by the 'hot phenol' method (Plant Tissue Culture Laboratory, University of Illinois-UC). The method worked in eliminating carbohydrate material present in the root tips. The integrity of the RNA was verified by denaturing agarose gels and spectrophotometry (ratio A260/A280). Poly(A)⁺mRNA was isolated twice from total RNA using the Oligotex Direct mRNA kit (Qiagen). Poly(A)⁺mRNA was converted to double-stranded cDNA and tagged by using modified Oligo(dT) primers. One of 4 sequence tags corresponding to a different segment of the root was added to the 3'-end of the modified Oligo(dT) primers, including a NotI site and used to reverse transcribe the segment-specific mRNAs into cDNAs. Each library contains all four tags. A suffix (s1, s2, s3, or s4) has been added to each sequence identifier to designate which region of the root (Root_segment_1, 2, 3, or 4) the sequence was found in based on the identification of the tag. A suffix of s0 indicates that the sequence tag, and hence the source segment, could not be identified. The double-stranded cDNAs were size-selected (>450 bp). Size selected cDNAs were adapted with EcoRI adaptors at both ends, and then digested with NotI. The cDNA was directionally cloned into EcoRI-NotI digested pBS 11 SK(+) phagemid vector (Stratagene) and electroporated into E.coli DH10B. The total number of white colony forming units (cfu) in the primary libraries before amplification was as follows: zmrw005: 3.37 x 10⁶; zmrw048: 4.87 x 10⁶; zmrw001: 3 x 10⁶. The background of empty clones was less than 1%. Inserts ranged from ~0.5kb to >2.5 kb, as determined by PCR. Plasmid DNA from the primary libraries then was converted to single-stranded circles and used as a template for PCR amplification using the T7 and T3 priming products, representing the entire cDNA population cloned in each library, were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 hours at 300°C. Non-hybridized single-stranded DNA circles were separated by electrophoresis into DH10B. The total number of clones with insert was: zmrw005: 2.0x10⁷; zmrw048: 4.2x10⁷; zmrw001: 1.1x10⁷. The background of empty clones was less than 2%. Insert size, determined by PCR of the entire library, ranged from 0.5kb to 2.5kb. (1) Sharp R E; Silk W K; Haioa T C. Growth of the Maize Primary Root at Low Water Potentials I. Spatial Distribution of Expansive Growth. Plant Physiology (Rockville). 87(1). 1988. 50-57. (2) Spollen W G; LeNoble M E; Samuels T D; Bernstein N; Sharp R E. Abscise acid accumulation maintains maize primary root elongation at low water potentials by restricting ethylene production. Plant Physiology (Rockville). 122(3). March, 2000. 967-976. TAG_SEQ=TCGCA"

```

Db      256 GTGTTGCTGCTGTGCTAGGCTTTGGTACGTATGGGCTTTATTGCTTCTGGAGTTGNGT 315
Qy      241 ACTACTTCGGTTGTTGTAATTATTATGANCAGTTCGGTATTCTTAATTCAGCTGGGCTACC 300
Db      316 ACTACTTCGGTTGTTGTAATTATTATNAGCAGTTCGGTATTGTAATTAGCTGGGCTACC 375
Qy      301 TGGACATTGTTATGATTATTAATAAATGCTTTGC 332
Db      376 TGGACATTGTTATGATTATTAATAAANGCTTGC 407

RESULT 13
LOCUS   BG841223
DEFINITION MEST19-A06.T3 ISUM4-TN Zea mays cDNA clone MEST19-A06 3', mRNA
sequence.
ACCESSION BG841223
VERSION   BG841223.2 GI:14243593
KEYWORDS EST.
SOURCE   Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 434)
Qiu,F., Cui,F., Guo,L., Ashlock,D.A., Wen,T.J. and Schnable,P.S.
Expressed Sequence Tags from B73 Maize Seedlings and Silks
Unpublished (2001)
On May 25, 2001 this sequence version replaced gi:14207545.
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
Tel: 515-294-0975
Fax: 515-294-5256
Email: schnable@iastate.edu
PCR PRimers
FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

FEATURES
            Location/Qualifiers
            1..434
                /organism="Zea mays"
                /mol_type="mRNA"
                /cultivar="B73"
                /db_xref="taxon:4577"
                /clone="MEST19-A06"
                /tissue_type="Seedling and silk"
                /lab_host="DH10B"
                /clone_lib="ISUM4-TN"
                /note="Vector: pT7T3PAC; Site 1: EcoRI; Site 2: NotI;
ds-cDNA molecules were generated as follows. First-strand
cDNA was prepared from oligo-dT selected mRNA by priming
with a NotI oligo-dT primer (5'
AACTGGAAGATTCCGCGCGCAGGAATTTTTTTTTTTTTTTT). The
resulting DNA:RNA hybrid was treated with Rnase H and used
as a template for DNA PolI-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pT7T3PAC vector. The library
then went through one round of normalization to Cot value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-806, 1996)."
```

ORIGIN

```

Query Match          97.1%; Score 319.4; DB 2; Length 434;
Best Local Similarity 98.8%; Pred. No. 1.2e-79;
Matches 320; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1  GGTGCGAGCGTGTGCTGTCCTGACGTTCTGCGCGCGCGGCTTTGGGCGCGCATC 60
Db      111 GGTGCGAGCGTGTGCTGTCCTGACGTTCTGCGCGCGCGGCTTTGGGCGCGCATC 170
```

```

Qy      61  AGAANC GTTGGTGGCTGTGCTGCTTCTGGTTTCTTTAA TTTTACCAAGTTTGT 120
Db      171 AGAAGCGTTCGCTGGGCTGTGCTGCTTCTGGTTTCTTTAA TTTTACCAAGTTTGT 230
Qy      121 CAAGGTGATCGCTGGTCAAGCCCGTGTCTTTAAANACCCACCGGCACTGGCAGTGA 180
Db      231 CAAGGTGATCGCTGGTCAAGGTCCGTGTCTTTAAAGACCCACCGGCACTGGCAGTGA 290
Qy      181 GTGTTGCTGCTTGTGTAGGCTTTGGTAGGTATGGGCTTTATTGCTTCTGATGTTGT 240
Db      291 GTGTTGCTGCTTGTGTAGGCTTTGGTAGGTATGGGCTTTATTGCTTCTGATGTTGT 350
Qy      241 ACTACTTGGGTTTGTGTAATTATTATGANCAGTTGCGTATTGTAATTCAGCTGGGCTACC 300
Db      351 ACTACTTGGGTTTGTGTAATTATTATGAGCAGTTGCGTATTGTAATTCAGCTGGGCTACC 410
Qy      301 TGGACATTGTTATGATTATTAATAA 324
Db      411 TGGACATTGTTATGATTATTAATAA 434

RESULT 14
LOCUS   CF625618/c
DEFINITION zmrws05_0A21-002-h12.s4 zmrws05 Zea mays cDNA 3', mRNA sequence.
ACCESSION CF625618
VERSION   CF625618.1 GI:37377941
KEYWORDS EST.
SOURCE   Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 629)
Bohnert,H., Sharp,R.E., Springer,G.K., Poroyko,V., Fredricksen,M.,
Sharp,L.G., Spollen,W.G., Ries,J., Guillen,A., Khambati,A.,
Topinka,C., Davis,G.E., Schachtman,D., Wu,Y. and Nguyen,H.T.
NSF Grant DBI-0211842: Functional Genomics of Root Growth and Root
Signaling Under Drought
Unpublished (2003)
Contact: Hans Bohnert
University of Illinois, Urbana-Champaign
1201 West Gregory Drive, Urbana, IL 61801, USA
Tel: 217-265-5475
Fax: 217-333-5574
Email: bohnert@life.uiuc.edu
POLYA=Yes.
```

FEATURES

```

            Location/Qualifiers
            1..629
                /organism="Zea mays"
                /mol_type="mRNA"
                /db_xref="taxon:4577"
                /clone_lib="zmrws05"
                /note="Samples were collected in Robert E. Sharp's lab
(University of Missouri-Columbia) to construct three
normalized cDNA libraries. Dark-grown maize seedlings with
primary roots 12-20 mm in length were transplanted to high
(-0.03 MPa) or low water potential (-1.6 MPa) vermiculite,
and harvested at 5 h and 48 h after transplanting. About
1,000 roots were used for each of the low water potential
libraries (zmrws05 and zmrws48) while 500 roots were
combined from each of the two time points at high water
potential (zmrws00). Each root was divided into 4 segments
(distances are from the junction of the root apex and root
cap): segment 1, 0-3 mm plus the root cap; segment 2, 3-7
mm; segment 3, 7-12 mm; segment 4, 12-20 mm. (For details
of conditions see (1) with nutrient modifications as in
(2)). The three normalized cDNA libraries were constructed
in the lab of Hans Bohnert (University of Illinois-UC).
Total RNA was extracted by the 'hot Phenol' method (Plant
Molecular Biology manual. D5: 1-13, 2nd ed., 1997). This
method worked in eliminating carbohydrate material present
```

in the root tips. The integrity of the RNA was verified by denaturing agarose gels and spectrophotometry (ratio A260/280). Poly(A)+mRNA was isolated twice from RNA using the Oligotex Direct mRNA kit (Qiagen). Poly(A)+mRNA was converted to double-stranded cDNA and tagged by using modified Oligo(dT) primers. One of 4 sequence tags corresponding to a different segment of the root was added to the 3'-end of the modified Oligo(dT) primers, including a NotI site and used to reverse transcribe the segment-specific mRNAs into cDNAs. Each library contains all four tags. A suffix (s1, s2, s3, or s4) has been added to each sequence identifier to designate which region of the root (Root segment 1, 2, 3, or 4) the sequence was found in based on the identification of the tag. A suffix of s0 indicates that the sequence tag, and hence the source segment, could not be identified. The double stranded cDNAs were size-selected (>450 bp). Size selected cDNAs were adaptor with EcoRI adaptors at both ends, and then digested with NotI. The cDNA was directionally cloned into EcoRI-NotI digested pBS II SK(+) phagemid vector (Stratagene) and electroporated into E.coli DH10B. The total number of white colony forming units (cfu) in the primary libraries before amplification was as follows: zmrw805: 3.37 x 10⁶; zmrw648: 4.87 x 10⁶; zmrw001: 3 x 10⁶. The background of empty clones was less than 1%. Inserts ranged from ~0.5kb to >2.5 kb, as determined by PCR. Plasmid DNA from the primary libraries then was converted to single-stranded circles and used as a template for PCR amplification using the T7 and T3 priming sites that flank the cloned cDNA inserts. The purified PCR products, representing the entire cDNA population cloned in each library, were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 hours at 300C. Non-hybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DH10B. The total number of clones with insert was: zmrw805: 2.0x10⁷; zmrw648: 4.2x10⁷; zmrw001: 1.1x10⁷. The background of empty clones was less than 2%. Insert size, determined by PCR of the entire library, ranged from 0.5kb to 2.5kb. (1) Sharp R E; Silk W K; Hsiao T C. Growth of the Maize Primary Root at Low Water Potentials I. Spatial Distribution of Expansive Growth. Plant Physiology (Rockville). 87(1). 1988. 50-57. (2) Spollen W G; LaNoble M E; Samuels T D; Bernstein N; Sharp R E. Abscissic acid accumulation maintains maize primary root elongation at low water potentials by restricting ethylene production. Plant Physiology (Rockville). 122(3). March, 2000. 967-976.

Db 114 ACTACTTGGGTTTGTGTAATTATTATGACAGTTGCGTATTGTAATTCAGCTGGGCTACC 55
Qy 300 CTGGACATTGTTATGTATTATAAATGCTTTGC 332
Db ||||||||||||||||||||||||||||| |||||
54 CTGGACATTGTTATGTATTATAAAGCTTTGC 22

Search completed: March 8, 2006, 05:42:24
Job time : 2670.19 secs

Result No.	Query			ID	Description
	Score	Match	Length		
1	329	100.0	332	7	US-10-603-524A-1
2	329	100.0	1236	7	US-10-425-114-13754
3	329	100.0	7545	9	US-10-508-166-10
4	329	100.0	11643	9	US-10-508-166-11
5	327.4	99.5	1206	7	US-10-425-114-32117
6	327.4	99.5	1271	7	US-10-425-114-3509
7	316.4	96.2	725	7	US-10-425-114-5169
8	315	95.7	526	7	US-10-425-114-5111
9	301.4	91.6	1294	8	US-10-739-930-3058
10	294	89.4	1057	7	US-10-425-114-1933
11	286	86.9	818	7	US-10-425-114-35874
12	278.4	84.6	458	7	US-10-425-114-5192
13	278.4	84.6	1216	7	US-10-425-114-25328
14	265.6	80.7	1391	8	US-10-425-115-153098
15	235.4	71.6	594	7	US-10-425-114-36047
16	232.6	70.7	1234	7	US-10-425-114-24766
17	232.6	70.7	1278	7	US-10-425-114-27672
18	204	62.0	1057	7	US-10-425-114-2886
19	187.8	57.1	325	8	US-10-425-115-65927
20	183.2	55.7	338	8	US-10-425-115-142679
21	169.4	51.5	611	8	US-10-425-115-108780
22	142	43.2	1203	8	US-10-425-115-156913
23	132.4	40.2	4708	8	US-10-425-115-119522
24	132.4	40.2	4203	8	US-10-425-115-119522
25	132.4	40.2	4203	8	US-10-425-115-119522
26	132.4	40.2	4203	8	US-10-425-115-119522
27	132.4	40.2	4203	8	US-10-425-115-119522
28	132.4	40.2	4203	8	US-10-425-115-119522
29	132.4	40.2	4203	8	US-10-425-115-119522
30	132.4	40.2	4203	8	US-10-425-115-119522
31	132.4	40.2	4203	8	US-10-425-115-119522
32	132.4	40.2	4203	8	US-10-425-115-119522
33	132.4	40.2	4203	8	US-10-425-115-119522
34	132.4	40.2	4203	8	US-10-425-115-119522
35	132.4	40.2	4203	8	US-10-425-115-119522
36	132.4	40.2	4203	8	US-10-425-115-119522
37	132.4	40.2	4203	8	US-10-425-115-119522
38	132.4	40.2	4203	8	US-10-425-115-119522
39	132.4	40.2	4203	8	US-10-425-115-119522
40	132.4	40.2	4203	8	US-10-425-115-119522
41	132.4	40.2	4203	8	US-10-425-115-119522
42	132.4	40.2	4203	8	US-10-425-115-119522
43	132.4	40.2	4203	8	US-10-425-115-119522
44	132.4	40.2	4203	8	US-10-425-115-119522
45	132.4	40.2	4203	8	US-10-425-115-119522
46	132.4	40.2	4203	8	US-10-425-115-119522
47	132.4	40.2	4203	8	US-10-425-115-119522
48	132.4	40.2	4203	8	US-10-425-115-119522
49	132.4	40.2	4203	8	US-10-425-115-119522
50	132.4	40.2	4203	8	US-10-425-115-119522
51	132.4	40.2	4203	8	US-10-425-115-119522
52	132.4	40.2	4203	8	US-10-425-115-119522
53	132.4	40.2	4203	8	US-10-425-115-119522
54	132.4	40.2	4203	8	US-10-425-115-119522
55	132.4	40.2	4203	8	US-10-425-115-119522
56	132.4	40.2	4203	8	US-10-425-115-119522
57	132.4	40.2	4203	8	US-10-425-115-119522
58	132.4	40.2	4203	8	US-10-425-115-119522
59</					

Db 121 CAAGGTGGATCGGTGGTCAAGCCGCTGTGCTTTAAANACCCACCGCACTGGCAGTGA 180
Qy 181 GTGTTGCTGCTGTAGGCTTTGTACGTATGGGCTTTATTTGCTTCTGGAATGTTGT 240
Db 181 GTGTTGCTGCTGTAGGCTTTGTACGTATGGGCTTTATTTGCTTCTGGAATGTTGT 240
Qy 241 ACTACTTGGGTTTGTGTAATTATTAATGANCAGTTCGGTATGTAATTCAGCTGGGCTACC 300
Db 241 ACTACTTGGGTTTGTGTAATTATTAATGANCAGTTCGGTATGTAATTCAGCTGGGCTACC 300
Qy 301 TGGACATTGTTATGTATTAATAAATGCTTTGC 332
Db 301 TGGACATTGTTATGTATTAATAAATGCTTTGC 332

RESULT 2

US-10-425-114-13754
; Sequence 13754, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 13754
; LENGTH: 1236
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB143-039-B10_FLI
US-10-425-114-13754

Query Match 100.0%; Score 329; DB 7; Length 1236;
Best Local Similarity 99.1%; Pred. No. 2.1e-89;
Matches 329; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGTCCAGCGTGTGCTGCTCGTACGTTCCTGCGCGCGCGGCTTTGGCGCGCGATC 60
Db 897 GGTCCAGCGTGTGCTGCTCGTACGTTCCTGCGCGCGCGGCTTTGGCGCGCGATC 956
Qy 61 AGAANCCTGCTGCTGCGGTGTGCTTCTGTTTGTCTTAATTTACCAAGTTTGT 120
Db 957 AGAAGCTGTGCTTGGCGGTGTGCTTCTGTTTGTCTTAATTTACCAAGTTTGT 1016
Qy 121 CAAGGTGGATCGGTGGTCAAGCCGCTGTGCTTTAAANACCCACCGCACTGGCAGTGA 180
Db 1017 CAAGGTGGATCGGTGGTCAAGCCGCTGTGCTTTAAAGACCCACCGCACTGGCAGTGA 1076
Qy 181 GTGTTGCTGCTGTAGGCTTTGTACGTATGGGCTTTATTTGCTTCTGGAATGTTGT 240
Db 1077 GTGTTGCTGCTGTAGGCTTTGTACGTATGGGCTTTATTTGCTTCTGGAATGTTGT 1136
Qy 241 ACTACTTGGGTTTGTGTAATTATTAATGANCAGTTCGGTATGTAATTCAGCTGGGCTACC 300
Db 1137 ACTACTTGGGTTTGTGTAATTATTAATGANCAGTTCGGTATGTAATTCAGCTGGGCTACC 300
Qy 301 TGGACATTGTTATGTATTAATAAATGCTTTGC 332
Db 1197 TGGACATTGTTATGTATTAATAAATGCTTTGC 1228

RESULT 3

US-10-508-166-10
; Sequence 10, Application US/10508166
; Publication No. US20050223430A1

; GENERAL INFORMATION:
; APPLICANT: PLANT RESEARCH INTERNATIONAL BV
; APPLICANT: BAKER, Hendrikus A.C.
; APPLICANT: FLORACK, Dionisius E.A.
; APPLICANT: BOSCH, Hendrik J.
; TITLE OF INVENTION: GNTIII expression in plants
; FILE REFERENCE: 62862A - P033313WO
; CURRENT APPLICATION NUMBER: US/10/508,166
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: US-60/365,769
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US-60/368,047
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 7545
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-508-166-10

Query Match 100.0%; Score 329; DB 9; Length 7545;
Best Local Similarity 99.1%; Pred. No. 4.7e-89;
Matches 329; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GGTCCAGCGTGTGCTGCTCGTACGTTCCTGCGCGCGCGGCTTTGGCGCGCGATC 60
Db 3273 GGTCCAGCGTGTGCTGCTCGTACGTTCCTGCGCGCGCGGCTTTGGCGCGCGATC 3332
Qy 61 AGAANCCTGCTGCTGCGGTGTGCTTCTGTTTGTCTTAATTTACCAAGTTTGT 120
Db 3333 AGAAGCTGTGCTTGGCGGTGTGCTTCTGTTTGTCTTAATTTACCAAGTTTGT 3392
Qy 121 CAAGGTGGATCGGTGGTCAAGCCGCTGTGCTTTAAANACCCACCGCACTGGCAGTGA 180
Db 3393 CAAGGTGGATCGGTGGTCAAGCCGCTGTGCTTTAAAGACCCACCGCACTGGCAGTGA 3452
Qy 181 GTGTTGCTGCTGTAGGCTTTGTACGTATGGGCTTTATTTGCTTCTGGAATGTTGT 240
Db 3453 GTGTTGCTGCTGTAGGCTTTGTACGTATGGGCTTTATTTGCTTCTGGAATGTTGT 3512
Qy 241 ACTACTTGGGTTTGTGTAATTATTAATGANCAGTTCGGTATGTAATTCAGCTGGGCTACC 300
Db 3513 ACTACTTGGGTTTGTGTAATTATTAATGANCAGTTCGGTATGTAATTCAGCTGGGCTACC 3572
Qy 301 TGGACATTGTTATGTATTAATAAATGCTTTGC 332
Db 3573 TGGACATTGTTATGTATTAATAAATGCTTTGC 3604

RESULT 4

US-10-508-166-11
; Sequence 11, Application US/10508166
; Publication No. US20050223430A1
; GENERAL INFORMATION:
; APPLICANT: PLANT RESEARCH INTERNATIONAL BV
; APPLICANT: BAKER, Hendrikus A.C.
; APPLICANT: FLORACK, Dionisius E.A.
; APPLICANT: BOSCH, Hendrik J.
; TITLE OF INVENTION: GNTIII expression in plants
; FILE REFERENCE: 62862A - P033313WO
; CURRENT APPLICATION NUMBER: US/10/508,166
; CURRENT FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: US-60/365,769
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US-60/368,047
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 11643

This Page Blank (uspto)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 04:19:11 ; Search time 885.156 Seconds
(without alignments)
865.410 Million cell updates/sec

Title: US-10-603-524A-1
Perfect score: 329
Sequence: 1 ggtcagcgtgctgctgc.....tgtattaataaagtgttgc 332

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7673375 seqs, 1153648444 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New.*

- 1: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq.*
- 2: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq.*
- 5: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq.*
- 6: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq.1*
- 7: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq.*
- 8: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq.1*
- 9: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq.2*
- 11: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq.3*
- 12: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq.4*
- 13: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	183	55.6	1676	9	US-11-096-568A-24715
2	36	10.9	567	6	Sequence 24715, A
3	35.8	10.9	582	6	Sequence 409218
4	35.8	10.9	583	6	Sequence 815284
5	35.6	10.8	568	6	Sequence 855422
6	35.4	10.8	568	6	Sequence 626220
7	35.4	10.8	568	6	Sequence 249647
8	35.4	10.8	6499	12	Sequence 249651
9	34.8	10.6	677	6	Sequence 91, Appl
10	34.8	10.6	677	6	Sequence 917185
11	34.8	10.6	33737	8	Sequence 917186
12	34.8	10.6	175100	12	US-10-276-233A-7
13	34.6	10.5	196716	9	US-11-121-086-21
14	33.8	10.3	63693	8	US-11-114-798-53
15	33.2	10.1	512	6	Sequence 53, Appl
16	33.2	10.1	546	6	Sequence 13269, A
17	33.2	10.1	612	6	Sequence 243873
18	33.2	10.1	630	6	Sequence 449515
19	33.2	10.1	630	6	Sequence 665533
20	33.2	10.1	735	6	Sequence 750364
					Sequence 750365
					Sequence 92022, A

C	21	33	10.0	196716	9	US-11-114-798-53	Sequence 53, Appl
	22	32.6	9.9	535	6	US-09-925-065A-51856	Sequence 51856, A
	23	32.6	9.9	578	6	US-09-925-065A-391285	Sequence 391285, A
	24	32.6	9.9	601	6	US-09-925-065A-729222	Sequence 729222, A
	25	32.6	9.9	627	6	US-09-925-065A-203360	Sequence 203360, A
	26	32.6	9.9	651	6	US-09-925-065A-888475	Sequence 888475, A
	27	32.4	9.8	529	6	US-09-925-065A-372789	Sequence 372789, A
	28	32.2	9.8	594	6	US-09-925-065A-882494	Sequence 882494, A
	29	32.2	9.8	595	6	US-09-925-065A-870022	Sequence 870022, A
	30	32	9.7	575	6	US-09-925-065A-662035	Sequence 662035, A
	31	32	9.7	575	6	US-09-925-065A-662036	Sequence 662036, A
	32	32	9.7	575	6	US-09-925-065A-662037	Sequence 662037, A
	33	32	9.7	599	6	US-09-925-065A-328191	Sequence 328191, A
	34	32	9.7	625	6	US-09-925-065A-866127	Sequence 866127, A
	35	32	9.7	1782	8	US-10-750-185-57415	Sequence 57415, A
	36	32	9.7	1782	8	US-10-750-623-57415	Sequence 57415, A
	37	31.8	9.7	344	6	US-09-925-065A-367472	Sequence 367472, A
	38	31.8	9.7	565	6	US-09-925-065A-357298	Sequence 357298, A
	39	31.8	9.7	640	6	US-09-925-065A-310742	Sequence 310742, A
	40	31.8	9.7	1691140	12	US-11-091-018-1	Sequence 1, Appl
	41	31.6	9.6	544	6	US-09-925-065A-89006	Sequence 89006, A
	42	31.6	9.6	544	6	US-09-925-065A-89007	Sequence 89007, A
	43	31.6	9.6	544	6	US-09-925-065A-89008	Sequence 89008, A
	44	31.6	9.6	672	6	US-09-925-065A-46570	Sequence 46570, A
	45	31.6	9.6	1080	7	US-10-932-182A-166756	Sequence 166756, A

ALIGNMENTS

RESULT 1

US-11-096-568A-24715
; Sequence 24715, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: Therby
; CURRENT APPLICATION NUMBER: US/11-096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 24715
; LENGTH: 1676
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1676)
; OTHER INFORMATION: Ceres Seq. ID no. 12450484
US-11-096-568A-24715

Query Match	55.6%	Score 183;	DB 9;	Length 1676;
Best Local Similarity	96.4%	Pred. No. 3.1e-42;		
Matches 186;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;
QY	140	AAGGCCCGTGTGCTTTAAANACCCGACCTGGCAGTGAGTGTGCTGTGTAGG	199	
Db	1476	AAGCCCGTGTGCTTTAAAGACCCACCGGACCTGGCAGTGAGTGTGCTGTGTAGG	1535	
QY	200	CTTTGGTACGTATGGGCTTTATTTGCTTCTCGAATGTTGTACTACTTGGGTTTGTGAA	259	
Db	1536	CTTTGGTACGTATGGGCTTTATTTGCTTCTCGAATGTTGTACTACTTGGGTTTGTGAA	1595	
QY	260	TTATATGACAGTTCGCTATTTGATTTACGTGGGCTACCTGGACATTTATATATTA	319	
Db	1596	TTATATGACAGTTCGCTATTTGATTTACGTGGGCTACCTGGACATTTATATATTA	1655	
QY	320	ATAAATGCTTTCG 332		
Db	1656	ATAAATGCTTTCG 1668		

```
RESULT 2
US-09-925-065A-409218/c
; Sequence 409218, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 409218
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-409218

Query Match      10.9%; Score 36; DB 6; Length 567;
Best Local Similarity 48.0%; Pred. No. 1.5;
Matches 96; Conservative 1; Mismatches 103; Indels 0; Gaps 0;

94 TTTGCTTTAATTTACCAAGTTGTTTCAAGTGGATCGGTGTCAGGCCCGGTGCT 153
239 TAGGTAATAGATTTTAAAGATGTTTAAAGGAGCTCAATGGTTAAAGTCAGCTTAA 180
154 TTAANACCCACCGCAGTGGCAGTGGTCTGCTGTGTAGCTTTGTGTACGTATG 213
179 TTAAGCCAGCATCAAGATGATGTGKTTGTGTGTGTGTATTTAAAG 120
214 GCCTTATTTGCTTCGGAATGTTGTACTACTTGGGTTTGTGAATATTATGANCAGT 273
119 GCCTTCATGTTGTTGTTTCTTCTCTAGGACCTTCTCTCTTTTGTGACCAA 60
274 TCGGTATTTGTAATTCAGCTG 293
59 AATGTTTTCTTCTCAGTTG 40

RESULT 3
US-09-925-065A-815284
; Sequence 815284, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 815284
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-815284

Query Match      10.9%; Score 35.8; DB 6; Length 582;
Best Local Similarity 49.7%; Pred. No. 1.7;
Matches 88; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

105 TTTACCAAGTTGTTTCAAGTGGATCGGTGTCAGGCCCGGTGCTTTAAANACCCA 164
186 TTTAAAAAGATTTTTTAAAGGAGCTCAATGGTTAAAGTCAGCTTAATTTAAAGCTAACA 245
165 CCGGCACCTGGCAGTGGTGTGCTGTGTAGCTTTGTGTACGTATGGGCTTTATTG 224
246 TCCAAGATGTGTGTGTATGTGTCATATGTGTGTGTATTATTAAAGGCTTTCAAG 305
225 CTTCGGAATGTTGTACTACTTGGGTTTGTGAATATTATGANCAGTTGCGTATT 281
306 TTTTGTCTTTTGTCTTCTCTAGGACCTTCTCTCTTTTGTGACCAAAAGTTTATT 362

RESULT 4
US-09-925-065A-855422
; Sequence 855422, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 855422
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-855422

Query Match      10.9%; Score 35.8; DB 6; Length 583;
Best Local Similarity 49.7%; Pred. No. 1.7;
Matches 88; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

105 TTTACCAAGTTGTTTCAAGTGGATCGGTGTCAGGCCCGGTGCTTTAAANACCCA 164
186 TTTAAAAAGATTTTTTAAAGGAGCTCAATGGTTAAAGTCAGCTTAATTTAAAGCTAACA 245
165 CCGGCACCTGGCAGTGGTGTGCTGTGTAGCTTTGTGTACGTATGGGCTTTATTG 224
246 TCCAAGATGTGTGTGTATGTGTCATATGTGTGTGTATTATTAAAGGCTTTCAAG 305
225 CTTCGGAATGTTGTACTACTTGGGTTTGTGAATATTATGANCAGTTGCGTATT 281
306 TTTTGTCTTTTGTCTTCTCTAGGACCTTCTCTCTTTTGTGACCAAAAGTTTATT 362

RESULT 5
US-09-925-065A-626220
; Sequence 626220, Application US/09925065A
; Publication No. US20040181048A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 10827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 626220
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-626220

Query Match      10.8%; Score 35.6; DB 6; Length 560;
Best Local Similarity 57.9%; Pred. No. 2;
Matches 62; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 212 TGGCGCTTATTGCTCTCGGATGTTGTGCTACTTGGTGTGTTGAATTATGACCA 271
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 191 TCGAATTATTATCTCTTTGATGTTGATTTAATTGGTTGCTAGTATTTTGGTGA 250
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 272 GTTGGCTATTGTAATTCAGCTGGCTACCTGACATTTGTTATGTATT 318
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 251 ATTTGCTGCTATTATCTGAGGTATCATCTGCTAGTTTTTTT 297
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
US-09-925-065A-249647
; Sequence 249647, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 10827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 249647
; LENGTH: 568
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-249647

Query Match      10.8%; Score 35.4; DB 6; Length 568;
Best Local Similarity 57.3%; Pred. No. 2.3;
Matches 63; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 209 GTATGGCTTTATTGCTTCTCGATGTTGTGCTACTTGGTGTGTTGAATTATGCA 268
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 383 GTTATGCTTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 442
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 269 NCAGTTGGCTATTGTAATTCAGCTGGCTACCTGACATTTGTTATGTATT 318
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 443 KCATGTGCTTACTTTATGACATAAGATGCTTTCAGGCTAAATTTTGTGTATT 492
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
US-09-925-065A-249651
; Sequence 249651, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 249651
; LENGTH: 568
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-249651

Query Match      10.8%; Score 35.4; DB 6; Length 568;
Best Local Similarity 57.3%; Pred. No. 2.3;
Matches 63; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 209 GTATGGCTTTATTGCTTCTCGATGTTGTGCTACTTGGTGTGTTGAATTATGCA 268
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 383 GTTATGCTTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 442
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 269 NCAGTTGGCTATTGTAATTCAGCTGGCTACCTGACATTTGTTATGTATT 318
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 443 KCATGTGCTTACTTTATGACATAAGATGCTTTCAGGCTAAATTTTGTGTATT 492
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
US-11-011-332A-91
; Sequence 91, Application US/11011332A
; Publication No. US20060024684A1
; GENERAL INFORMATION:
; APPLICANT: Foekens, John
; APPLICANT: Harbeck, Nadia
; APPLICANT: Koenig, Thomas
; APPLICANT: Maier, Sabine
; APPLICANT: Martens, John
; APPLICANT: Model, Fabian
; APPLICANT: Nimrich, Inko
; APPLICANT: Rujan, Tamas
; APPLICANT: Schmitt, Manfred
; APPLICANT: Lesche, Ralf
; APPLICANT: Dietrich, Dimo
; APPLICANT: Mueller, Volkmar
; APPLICANT: Kluth, Antje
; APPLICANT: Schwöpe, Ina
; APPLICANT: Hartmann, Oliver
; APPLICANT: Adorjan, Peter
; TITLE OF INVENTION: PROGNOSTIC MARKERS FOR PREDICTION OF TREATMENT RESPONSE AND/OR SURVIVAL IN BREAST CANCER PATIENTS
; FILE REFERENCE: 47675-99
```



```
; CURRENT APPLICATION NUMBER: US/11/011.332A
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US 10/517,741
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: PCT/EP2004/014170
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: EP 03090432.0
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: EP 04090041.7
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: EP 04090380.9
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: EP 04090127.4
; PRIOR FILING DATE: 2004-04-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 91
; LENGTH: 6499
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-11-011-332A-91

Query Match          10.8%; Score 35.4; DB 12; Length 6499;
Best Local Similarity 46.8%; Pred. No. 4.6;
Matches 108; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

Qy      88  TTCTGTTTGGCTTTAAATTTACCAAGTTTGTTCAGGTGGATCCGTTGTCAGGCGCG 147
Db      88  TTTTGTGGATGGTTGTAATTTTGTGGAGTGGTTATAGAGGTGTGATTTTGTG 3663

Qy      148  TTGCTTTAAANACCCACCGCAGTGGCAGTGGTGTCTGTGTAGCTTTTGTA 207
Db      148  TATGAGGTAAGGTAAGATTAATGATATAGTTATGATAGAGGTGTGATTTTGTG 3723

Qy      208  CGTATGGCTTTATTTGCTTCGATGTTGTACTACTGCTGGTTGTTGTAATTAATG 267
Db      208  TTTTGTGGATGGTTGTAATTTTGTGGAGTGGTTATAGAGGTGTGATTTTGTG 3723

Qy      3724  TTAATAATTTTGATTTATTAATGTAAGTTTGTGTTTAAATTTGTTTTTGGAGTATTAATG 3783
Db      3724  TTAATAATTTTGATTTATTAATGTAAGTTTGTGTTTAAATTTGTTTTTGGAGTATTAATG 3783

Qy      268  ANCAGTTCGTATTTGTAATTCAGCTGGGCTACCTCGACATGTTATGTAAT 318
Db      268  TTTTGTGGATGGTTGTAATTTTGTGGAGTGGTTATAGAGGTGTGATTTTGTG 3834

RESULT 9
US-09-925-065A-917185
; Sequence 917185, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 10827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 917186
; LENGTH: 677
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-917186

Query Match          10.6%; Score 34.8; DB 6; Length 677;
Best Local Similarity 60.0%; Pred. No. 3.5;
Matches 57; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy      17  TGTCCGTGCTACGTTCTGGCGCGCGGCTTGGCGCGGATCAGAACCTTCGTTGG 76
Db      17  TGTCCGTGCTACGTTCTGGCGCGCGGCTTGGCGCGGATCAGAACCTTCGTTGG 76

Qy      479  TGTGAGCTGCTCTTCAGGACAGCTGGGCCAAGGATGCTGGAGCTCAGACCTTCAGTGG 538
Db      479  TGTGAGCTGCTCTTCAGGACAGCTGGGCCAAGGATGCTGGAGCTCAGACCTTCAGTGG 538

Qy      77  CGTGTGTGCTCTCTGCTTTGCTTTAAATTTTACCA 111
Db      77  CGTGTGTGCTCTCTGCTTTGCTTTAAATTTTACCA 111

Qy      539  GGTCTGTGCTCTGCTGCTCAACGTCATTCCTCCCA 573
Db      539  GGTCTGTGCTCTGCTGCTCAACGTCATTCCTCCCA 573

RESULT 10
US-09-925-065A-917186
; Sequence 917186, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 10827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 917186
; LENGTH: 677
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-917186

Query Match          10.6%; Score 34.8; DB 6; Length 677;
Best Local Similarity 60.0%; Pred. No. 3.5;
Matches 57; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy      17  TGTCCGTGCTACGTTCTGGCGCGCGGCTTGGCGCGGATCAGAACCTTCGTTGG 76
Db      17  TGTCCGTGCTACGTTCTGGCGCGCGGCTTGGCGCGGATCAGAACCTTCGTTGG 76

Qy      479  TGTGAGCTGCTCTTCAGGACAGCTGGGCCAAGGATGCTGGAGCTCAGACCTTCAGTGG 538
Db      479  TGTGAGCTGCTCTTCAGGACAGCTGGGCCAAGGATGCTGGAGCTCAGACCTTCAGTGG 538

Qy      77  CGTGTGTGCTCTCTGCTTTGCTTTAAATTTTACCA 111
Db      77  CGTGTGTGCTCTCTGCTTTGCTTTAAATTTTACCA 111

Qy      539  GGTCTGTGCTCTGCTGCTCAACGTCATTCCTCCCA 573
Db      539  GGTCTGTGCTCTGCTGCTCAACGTCATTCCTCCCA 573

RESULT 11
US-10-276-233A-7
; Sequence 7, Application US/10276233A
; Publication No. US20050260572A1
; GENERAL INFORMATION:
; APPLICANT: Hitachi Software Engineering Co., Ltd.
; TITLE OF INVENTION: A method of predicting cancer condition
; FILE REFERENCE: PH-1533-PCT
```

```
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 917185
; LENGTH: 677
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-917185

Query Match          10.6%; Score 34.8; DB 6; Length 677;
Best Local Similarity 60.0%; Pred. No. 3.5;
Matches 57; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy      17  TGTCCGTGCTACGTTCTGGCGCGCGGCTTGGCGCGGATCAGAACCTTCGTTGG 76
Db      17  TGTCCGTGCTACGTTCTGGCGCGCGGCTTGGCGCGGATCAGAACCTTCGTTGG 76

Qy      479  TGTGAGCTGCTCTTCAGGACAGCTGGGCCAAGGATGCTGGAGCTCAGACCTTCAGTGG 538
Db      479  TGTGAGCTGCTCTTCAGGACAGCTGGGCCAAGGATGCTGGAGCTCAGACCTTCAGTGG 538

Qy      77  CGTGTGTGCTCTCTGCTTTGCTTTAAATTTTACCA 111
Db      77  CGTGTGTGCTCTCTGCTTTGCTTTAAATTTTACCA 111

Qy      539  GGTCTGTGCTCTGCTGCTCAACGTCATTCCTCCCA 573
Db      539  GGTCTGTGCTCTGCTGCTCAACGTCATTCCTCCCA 573

RESULT 10
US-09-925-065A-917186
; Sequence 917186, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 10827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 917186
; LENGTH: 677
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-917186

Query Match          10.6%; Score 34.8; DB 6; Length 677;
Best Local Similarity 60.0%; Pred. No. 3.5;
Matches 57; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy      17  TGTCCGTGCTACGTTCTGGCGCGCGGCTTGGCGCGGATCAGAACCTTCGTTGG 76
Db      17  TGTCCGTGCTACGTTCTGGCGCGCGGCTTGGCGCGGATCAGAACCTTCGTTGG 76

Qy      479  TGTGAGCTGCTCTTCAGGACAGCTGGGCCAAGGATGCTGGAGCTCAGACCTTCAGTGG 538
Db      479  TGTGAGCTGCTCTTCAGGACAGCTGGGCCAAGGATGCTGGAGCTCAGACCTTCAGTGG 538

Qy      77  CGTGTGTGCTCTCTGCTTTGCTTTAAATTTTACCA 111
Db      77  CGTGTGTGCTCTCTGCTTTGCTTTAAATTTTACCA 111

Qy      539  GGTCTGTGCTCTGCTGCTCAACGTCATTCCTCCCA 573
Db      539  GGTCTGTGCTCTGCTGCTCAACGTCATTCCTCCCA 573

RESULT 11
US-10-276-233A-7
; Sequence 7, Application US/10276233A
; Publication No. US20050260572A1
; GENERAL INFORMATION:
; APPLICANT: Hitachi Software Engineering Co., Ltd.
; TITLE OF INVENTION: A method of predicting cancer condition
; FILE REFERENCE: PH-1533-PCT
```

; CURRENT APPLICATION NUMBER: US/10/276,233A
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: JP 2001-73063
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: JP 2001-108503
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: JP 2001-234807
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in Ver. 3.2
; SEQ ID NO 7
; LENGTH: 33737
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-233A-7

Query Match 10.6%; Score 34.8; DB 8; Length 33737;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 57; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 17 TGTGGTGTAGCTTCTGGCGCGCGGCTTGGGCGCGGATCAGAACGTTGGCTGG 76
Db 26246 TGTGAGCTGCTCTTCCAGACAGCTGGGCGCAAGGATGCTGGAGCTCAGACCTTGCAGTGG 26305
QY 77 CCGTGTGTGCTCTGCTTGTCTTAAATTTACCA 111
Db 26306 GGTCTGTGCTCTGTGTCAAGTCAATCTTCCCA 26340

RESULT 12

US-11-121-086-21
; Sequence 21, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: NIELSEN, KIRSTEN V.
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.5000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 21
; LENGTH: 175100
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-21

Query Match 10.6%; Score 34.8; DB 12; Length 175100;
Best Local Similarity 60.0%; Pred. No. 18;
Matches 57; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 17 TGTGGTGTAGCTTCTGGCGCGCGGCTTGGGCGCGGATCAGAACGTTGGCTGG 76
Db 79714 TGTGAGCTGCTCTTCCAGACAGCTGGGCGCAAGGATGCTGGAGCTCAGACCTTGCAGTGG 79773
QY 77 CCGTGTGTGCTCTGCTTGTCTTAAATTTACCA 111
Db 79774 GGTCTGTGCTCTGTGTCAAGTCAATCTTCCCA 79808

RESULT 13

US-11-114-798-53
; Sequence 53, Application US/11114798
; Publication No. US20060035246A1
; GENERAL INFORMATION:
; APPLICANT: WU, RINA
; APPLICANT: MARQUEZ, ABBEY
; TITLE OF INVENTION: CHROMOGENIC IN SITU HYBRIDIZATION METHODS, KITS, AND
; FILE REFERENCE: 0618.011.0004

; CURRENT APPLICATION NUMBER: US/11/114,798
; CURRENT FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: 10/173,525
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/952,851
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patent in Ver. 3.3
; SEQ ID NO 53
; LENGTH: 196716
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-11-114-798-53

Query Match 10.5%; Score 34.6; DB 9; Length 196716;
Best Local Similarity 57.5%; Pred. No. 22;
Matches 61; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 216 CTTTATTTGCTTCTCGATGTTGTGTACTACTTGGCTTTGTTGAAATTAATGACAGTTG 275
Db 31777 CATAATAGGTGTAGATTGTCAATGCTTTTTCATCAATTAATATCATATG 31836
QY 276 CGTATTGTAATTCAGCTGGCTACCTGGACATTTGTTATGTATTAAT 321
Db 31837 ATCCCTTCTAATTCAGCTGTTGATATGTTGGATCACAATGATTGAT 31882

RESULT 14

US-10-995-561-13269
; Sequence 13269, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13269
; LENGTH: 63693
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13269

Query Match 10.3%; Score 33.8; DB 8; Length 63693;
Best Local Similarity 48.6%; Pred. No. 26;
Matches 118; Conservative 0; Mismatches 124; Indels 1; Gaps 1;
QY 84 GTGCTTCTGGTTGCTTTAAATTTTACCAAGTTTGTTCAGGTGGATCCGCTGCAAGG 143
Db 48715 GAGATTCCTGGTATGTTGTATCTTTATCTCATTAGTTCAGAGAACTTCTCTGATTTTC-TGC 48773
QY 144 CCGGTGCTCTTAAANACCCACCGCACTGGCAGTGTGCTGCTGTGTAGCTTTT 203
Db 48774 CATAATTTCAATTAATTCACCCAAAAGTCATTGAGGAGCATTTGTTTGTATTCATGTAAT 48833
QY 204 GGTAGTATGGCTTTTATTTGCTCTGATGTTGTGTACTACTTCTGGTTTGTGAATTAAT 263
Db 48834 TGTACGGTTTGTAGTTATTTTCTTAGTCTTGATGCTGATTTCAATTTGCTGTGGTCTGAG 48893
QY 264 TATGANCAGTTGCGTATTGTAATTCAGCTGGGCTACCTGGACATTTGTTATGTAATAA 323
Db 48894 AGTGTGTTTGGTATGATTTTGTCTTCTTGGCACCTGCTGAAGATGTTTATGTCCAATT 48953
QY 324 ATG 326
Db 48954 ATG 48956

GenCore version 5.1.7
Copyright (C) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 23:00:44 ; Search time 139.621 Seconds
(without alignments)
4226.797 Million cell updates/sec

Title: US-10-603-524A-1

Perfect score: 329

Sequence: 1 ggtcagcgtgtgctgtc.....tgtattataaatgctttgc 332

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/1_COMB.seq:*
- 2: /cgn2_6/prodata/1/ina/5_COMB.seq:*
- 3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/prodata/1/ina/H_COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*
- 7: /cgn2_6/prodata/1/ina/PP_COMB.seq:*
- 8: /cgn2_6/prodata/1/ina/RE_COMB.seq:*
- 9: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	27.7	1333	2	US-08-288-630-1
2	84.8	25.8	758	2	US-08-288-630-1
3	76.6	23.3	291	3	US-09-313-294A-6335
4	37.6	11.4	67643	3	US-09-949-016-14760
5	35.4	10.8	17146	3	US-09-949-016-16774
6	34.8	10.6	100990	3	US-09-409-800B-2
7	34.2	10.4	126176	3	US-09-949-016-16137
8	34.2	10.4	126176	3	US-09-949-016-16138
9	34.2	10.4	451924	3	US-09-949-016-12896
10	34.2	10.4	451925	3	US-09-949-016-17305
11	33.8	10.3	924	3	US-09-248-798A-1471
12	33.8	10.3	55195	3	US-09-949-016-15854
13	33.2	10.1	300598	3	US-09-949-016-11868
14	33.2	10.1	308362	3	US-09-949-016-17119
15	33.2	10.1	4403765	3	US-09-103-840A-2
16	33.2	10.1	4411529	3	US-09-103-840A-1
17	33	10.0	70000	3	US-09-851-896-3
18	33	10.0	76399	3	US-09-949-016-16819
19	33	10.0	146307	3	US-09-949-016-14881
20	33	10.0	146307	3	US-09-949-016-14882
21	33	10.0	146307	3	US-09-949-016-14883
22	33	10.0	146307	3	US-09-949-016-14884
23	33	10.0	146307	3	US-09-949-016-14885
24	33	10.0	146307	3	US-09-949-016-14886

C 25	33	10.0	146307	3	US-09-949-016-14887
C 26	33	10.0	146307	3	US-09-949-016-14888
C 27	33	10.0	148405	3	US-09-949-016-11747
C 28	33	10.0	148405	3	US-09-949-016-12835
C 29	33	10.0	148405	3	US-09-949-016-12836
C 30	33	10.0	148405	3	US-09-949-016-12837
C 31	32.6	9.9	26134	3	US-09-949-016-15285
C 32	32.6	9.9	145812	3	US-09-949-016-15698
C 33	32.6	9.9	767677	3	US-09-949-016-12147
C 34	32.6	9.9	767677	3	US-09-949-016-17361
C 35	32.4	9.8	399	3	US-09-621-976-8976
C 36	32	9.7	13015	3	US-09-639-207-10
C 37	31.6	9.6	288	3	US-09-513-999C-2582
C 38	31.6	9.6	10758	3	US-08-956-171E-221
C 39	31.6	9.6	10758	3	US-08-781-986A-221
C 40	31.6	9.6	26867	3	US-09-949-016-16332
C 41	31.6	9.6	26867	3	US-09-949-016-16333
C 42	31.6	9.6	285986	3	US-09-949-016-12287
C 43	31.6	9.6	288031	3	US-09-949-016-14864
C 44	31.4	9.5	400	3	US-08-956-171E-4132
C 45	31.4	9.5	400	3	US-08-781-986A-4132

ALIGNMENTS

RESULT 1
US-08-288-630-1
; Sequence 1, Application US/08288630
; Patent No. 5837848
; GENERAL INFORMATION:
; APPLICANT: ELY, SUSAN
; APPLICANT: EVANS, IAN J
; APPLICANT: SCHUCH, WOLFGANG W
; TITLE OF INVENTION: ROOT-SPECIFIC PROMOTER
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,630
; FILING DATE: 10-AUG-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/111,590
; FILING DATE: 25-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/669,433
; FILING DATE: 15-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9006017.9
; FILING DATE: 16-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 215964/SEE35669USCIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1333 base pairs
; TYPE: nucleic acid

Sequence 14887, A
Sequence 14888, A
Sequence 11747, A
Sequence 12835, A
Sequence 12836, A
Sequence 12837, A
Sequence 15285, A
Sequence 15698, A
Sequence 12147, A
Sequence 17361, A
Sequence 8976, Ap
Sequence 10, Appl
Sequence 2582, Ap
Sequence 221, App
Sequence 221, App
Sequence 16332, A
Sequence 16333, A
Sequence 12287, A
Sequence 14864, A
Sequence 4132, Ap
Sequence 4132, Ap

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-288-630-1

Query Match 27.7%; Score 91; DB 2; Length 1333;
Best Local Similarity 64.7%; Pred. No. 5.1e-20;
Matches 211; Conservative 0; Mismatches 83; Indels 32; Gaps 4;

QY 22 GTCGACGCTTCTGGCGCGCGCTTGGCGCGCGGATCAGAANGTTGGCGTGTG 81
DB 995 GTCGACGTCGACGCGTCTCTGGCGCGCGGATCAGAANGTTGGCGTGTG 1054

QY 82 GTGTGCTTCTGGTTGCTTAATTTTACC--AAGTTTGTTCAGGTGGATCGCTGTGTC 139
DB 1055 TGTGTGTGGGTCTGGTTGCTTTTACCAAAAGTTTGTTCAGAGTGGATCGCTGTGTC 1114

QY 140 AAGGCCCGTGTGCTTTA-----AANACCACCGGCACTGGCAGTGAAGTTGCTGCTTG 193
DB 1115 AAGTCCGCTGTCTATTAAAGTGGATCGCGTGAATCTGGCAGTGAAGTTGCTGCTTG 1174

QY 194 TGTAGGCTTGGTAGTATGGCTTTATTTGCTTCTGA----- 232
DB 1175 TGTAGGCTGCTAGTACGCGGCTTTATTTTGGTCCCAAGTCAAAAGTCAAGTGGTCT 1234

QY 233 TGTGTGTACTACTGGCTTGTGAATATTATGANCAGTTGCGTATTTGAATTCAGCT 292
DB 1235 GGAATGCTGTACTTGGGTTTGTGA---ATTATGAGCAGCTGGCGTGTGTAAATTCGCT 1291

QY 293 GGGCTACCTGGACATTTATGTATT 318
DB 1292 GGGCTACCTGGATCGGTTAATAATT 1317

RESULT 2
US-08-288-630-2/c
; Sequence 2, Application US/08288630
; Patent No. 5837848
; GENERAL INFORMATION:
; APPLICANT: ELY, SUSAN
; APPLICANT: EVANS, IAN J
; APPLICANT: SCHUCH, WOLFGANG W
; TITLE OF INVENTION: ROOT-SPECIFIC PROMOTER
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,630
; FILING DATE: 10-AUG-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/111,590
; FILING DATE: 25-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/669,433
; FILING DATE: 15-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9006017.9
; FILING DATE: 16-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 215964/SBB35669USCIP

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 758 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-288-630-2

Query Match 25.8%; Score 84.8; DB 2; Length 758;
Best Local Similarity 68.2%; Pred. No. 4.4e-18;
Matches 202; Conservative 0; Mismatches 61; Indels 33; Gaps 5;

QY 38 GGCGCGGCTTGGCGCGGATCAGAANCCTGGCTTGGCGGTGTGTGCTTCTGCTTTG 97
DB 440 GTCCTGCGGTGGCGCGGATTAGAAGC-TAGCTAGCGTTGGCATGTGTGCTTCT 382

QY 98 CTTTAAATTTTACC--AAGTTTGTTCAGGTGGATCGGTGTCAGGCCCGTGTGCTTT 155
DB 381 GTTGTGCTTTTACCAAAAGTTTGTTCAGGTGGATCGCTGCTCAAGTCCGTGTGCTCT 322

QY 156 AANAC-----CCACCGGCACTGGCAGTGAAGTCTGCTGTAGGCTTTGGTACG 209
DB 321 ATTAAGTGGATCGGTGACTCTGGCAGTGAAGTCTGCTGTAGGACGTTGTTACG 262

QY 210 TATGGGCTTTATTTGCTTCTGA-----TGTGTGTACTACTTTG 248
DB 261 TACGGGCTTTATTTGTTCCCAAGTCAAAAGTCAAGTCTGGATGTGTGTACTTTG 202

QY 249 GGTGTGTGAATTTATGANCAGTTGCGTATTGTAATTCAGTCTGGGCTACTCTGA 304
DB 201 GGTGTGTGA---ATTATGAGCAGTCTGCTGTGTAAATTCGGCTGGGCTACTCTGA 149

RESULT 3
US-09-313-294A-6335
; Sequence 6335, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 6335
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700351622H1
; NAME/KEY: unsure
; LOCATION: 17
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-6335

Query Match 23.3%; Score 76.6; DB 3; Length 291;
Best Local Similarity 76.4%; Pred. No. 1.5e-15;
Matches 146; Conservative 0; Mismatches 36; Indels 9; Gaps 4;

QY 38 GGCGCGGCTTGGCGCGGATCAGAANCCTGGCTTGGCGGTGTGTGCTTCTGCTTT 95
DB 69 GGCGCGGCTTGGCGGATC-AGAAGTAGTGTGGCATGTGGGTTCTGGTTCTGTT 127
QY 96 TGCTTTAATTTTACCAAGTTTGTTCAGGTGGATCGGTGCTCAAGGCCCGTGTGCTTT 155


```
; Sequence 16137, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16137
; LENGTH: 126176
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16137

Query Match 10.4%; Score 34.2; DB 3; Length 126176;
Best Local Similarity 57.7%; Pred. No. 6.6;
Matches 60; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 215 GCTTATTGCTCTCGGATGTTGTACTACTTGGTTTGTGAATTATTATGANCAGTT 274
DB 121156 GGTGATTATGTTTTTGTGATGCTCTGGATTCCGATTGGTAGTATTTTGTGAAAAATT 121215

QY 275 GCGTATTGTAATTCAGCTGGGCTACTCGACATCTGTAATGATT 318
DB 121216 TTGCATCTGTCTCATCAGGATATGCTCTATAGTTTTTGT 121259

RESULT 8
US-09-949-016-16138
; Sequence 16138, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16138
; LENGTH: 126176
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16138

Query Match 10.4%; Score 34.2; DB 3; Length 126176;
Best Local Similarity 57.7%; Pred. No. 6.6;
Matches 60; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 215 GCTTATTGCTCTCGGATGTTGTACTACTTGGTTTGTGAATTATTATGANCAGTT 274
DB 121156 GGTGATTATGTTTTTGTGATGCTCTGGATTCCGATTGGTAGTATTTTGTGAAAAATT 121215

QY 275 GCGTATTGTAATTCAGCTGGGCTACTCGACATCTGTAATGATT 318
DB 121216 TTGCATCTGTCTCATCAGGATATGCTCTATAGTTTTTGT 121259

RESULT 9
US-09-949-016-12896
; Sequence 12896, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12896
; LENGTH: 451924
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12896

Query Match 10.4%; Score 34.2; DB 3; Length 451924;
Best Local Similarity 57.7%; Pred. No. 13;
Matches 60; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 215 GCTTATTGCTCTCGGATGTTGTACTACTTGGTTTGTGAATTATTATGANCAGTT 274
DB 340246 GGTGATTATGTTTTTGTGATGCTCTGGATTCCGATTGGTAGTATTTTGTGAGGATTA 340305

QY 275 GCGTATTGTAATTCAGCTGGGCTACTCGACATCTGTAATGATT 318
DB 340306 TTGTGTTTACATTTCATCAGGATATGGCCTATAGTTTCTATT 340349

RESULT 10
US-09-949-016-17305
; Sequence 17305, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17305
; LENGTH: 451925
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17305

Query Match 10.4%; Score 34.2; DB 3; Length 451925;
Best Local Similarity 57.7%; Pred. No. 13;
Matches 60; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 215 GCTTATTGCTCTCGGATGTTGTACTACTTGGTTTGTGAATTATTATGANCAGTT 274
DB 340246 GGTGATTATGTTTTTGTGATGCTCTGGATTCCGATTGGTAGTATTTTGTGAGGATTA 340305

QY 275 GCGTATTGTAATTCAGCTGGGCTACTCGACATCTGTAATGATT 318
```


Db	44689	GAGATTCGGTAGTGTATCTTTATTTCTCATTTCAAGAACTTCCTGATTC-TGC	44747
Qy	144	CCCGTGTGCTTTAAANACCCACCGGACCTGGCAGTGAGTGTGTGCTGTGTGTAGGCTTT	203
Db	44748	CATAATTTCAATTAATTCACCCAAAAGTCATTCAGGAGCATGTGTTTGATTTCCATGTAAT	44807
Qy	204	GGTACGTATGGCGCTTATTTTGCTCTCGATGTTGTGTACTACTTGGGTTTTGTTGAATTAAT	263
Db	44808	TGTACGGTTTGAGTATATTTTCTTAGTCTTGACTGTTATTCATGTGCTGTGGTCTGAG	44867
Qy	264	TATGANCAGTTCGGTATTGTGTAATTCAGCTGGGCTACCTGGACATTGTTATGTATTATAAA	323
Db	44868	AGTGTGTTTTGGTATGATTTTGTTGTTCTTTGGCATTGCTGAAAGATGTTTTATGTCCAAT	44927
Qy	324	ATG 326	
Db	44928	ATG 44930	

RESULT 13
US-09-949-016-11868/c
; Sequence 11868, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE. METHODS OF DETECTION AND USES THEREOF

```

; AFFILIATION: VEMIER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11868
; LENGTH: 300598

```

RESULT 12
US-09-949-016-15854
; Sequence 15854, Application US/09949016
; Patent NO. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1-001307

Query Match	10.1%;	Score 33.2;	DB 3;	Length 300598;
Best Local Similarity	51.0%;	Pred. No. 23;		
Matches	77;	Conservative 0;	Mismatches 74;	Indels 0; Gaps 0;
Qy	172	TGGCAGTGACGTGTCTGTGTGTAGCGCTTTGGTACGTATGGCGCTTTATTGCTTCTGG	231	
Db	256664	TGTGTGTGTGTGTGTGTGTGTGTATTAAAGAACATGGTGTTTATATACTCTGCA	256605	
Qy	232	ATGTGTGTACTACTCTGGGTTTGTGAATTATTATGANCACGTTCGGTATGTAAATTCAGC	291	
Db	256604	GTGGTATCAAGAATGCGCTTTGTGAATTGCACCTTAATAGATTTTTTTTTCGCATCTGG	256545	
Qy	292	TGGGCTACCTGGACATTTGTATGATTAAATA	322	
Db	256544	AACTTCATGTCGCAATTTTGTGGTTTAA	256514	

RESULT 14
US-09-949-016-17119/c
; Sequence 17119, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN
GENES ASSOCIATED

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 04:07:00 ; Search time 2337.81 Seconds
(without alignments)
5823.847 Million cell updates/sec

Title: US-10-603-524A-2
Perfect score: 291
Sequence: 1 agccggcttatgtcgtag.....tgtgagtggtctatatcaaa 291

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_hc:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_est7:
9: gb_gsa1:
10: gb_gsa2:
11: gb_gsa3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	287.8	98.9	692	DN204218	MEST801.D
C 2	285.8	98.2	451	CF626836	zmrw805_0
C 3	285.8	98.2	675	CF627673	zmrw805_0
C 4	284.6	97.8	448	BE639295	946020E02
C 5	282.6	97.1	404	CF061011	QCT16d11
C 6	281	96.6	437	CF061154	QCT18c03
C 7	279.8	96.2	313	BM888666	952067R09
C 8	279.8	96.2	313	BM895191	952066H10
C 9	279.8	96.2	599	AI738207	606047B11
C 10	278.2	95.6	628	AW061962	687009G02
C 11	276.8	95.1	290	BQ163609	952077G01
C 12	276.6	95.1	409	BQ163007	952032D09
C 13	276.6	95.1	461	AW519844	660053H10
C 14	270.6	93.0	289	DN217785	MEST800.E
C 15	270.6	93.0	290	DN223333	MEST1144
C 16	270.4	92.9	280	BE186822	946012H04
C 17	267.8	92.0	312	BM888756	952068H02
C 18	266.8	91.7	619	AW191435	687028F09
C 19	265.6	91.3	614	BU079762	946147C04
C 20	264	90.7	329	BM498022	952032D09
C 21	263.8	90.7	295	DR906452	E0808 Zea
C 22	262.8	90.3	424	BI180447	949036H01

23	261.4	89.8	273	3	BM896196	BM896196	952067H02
C 24	260.2	89.4	342	1	AI619189	AI619189	486086F12
C 25	260.2	89.4	468	2	BG840667	BG840667	MEST14-F0
C 26	260.2	89.4	468	3	BG841013	BG841013	MEST14-F0
C 27	260.2	89.4	536	2	BM381193	BM381193	MEST531-C
C 28	260.2	89.4	548	3	BM380521	BM380521	MEST531-B
C 29	260.2	89.4	556	3	BM382000	BM382000	MEST543-B
C 30	260.2	89.4	602	1	AI621840	AI621840	486027B11
C 31	260.2	89.4	625	8	DN229243	DN229243	MEST1014
C 32	260.2	89.4	629	1	AI622731	AI622731	486106A12
C 33	260.2	89.4	644	6	CA402201	CA402201	EL01N0433
C 34	260.2	89.4	650	8	CA402201	CA402201	EL01N0433
C 35	260.2	89.4	661	6	CD434915	CD434915	MEST1111
C 36	260.2	89.4	716	8	DN223155	DN223155	EL01N0330
C 37	260.2	89.4	719	8	DN2221819	DN2221819	MEST1138
C 38	260.2	89.4	735	6	BZ622915	BZ622915	MEST1120
C 39	260.2	89.4	815	6	CD445358	CD445358	EL01N0450
C 40	258.8	88.9	595	5	BU572123	BU572123	946168C02
C 41	258.6	88.9	537	3	BM074032	BM074032	MEST79-C0
C 42	258.6	88.9	634	7	CO529353	CO529353	3530.1.19
C 43	258.6	88.9	652	3	BM380681	BM380681	MEST523-D
C 44	258.4	88.8	270	3	BM896245	BM896245	952068E09
C 45	258.4	88.8	270	3	BQ035196	BQ035196	952077G01

ALIGNMENTS

RESULT 1
DN204218/c
LOCUS DN204218 692 bp mRNA linear EST 28-FEB-2005
DEFINITION MEST801.D04.T7-1 UGA-ZmSAM-X22 Zea mays cDNA, mRNA sequence.
ACCESSION DN204218
VERSION DN204218.1 GI:60337245
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
1 (bases 1 to 692)
Chen,H.D., Zhang,X., Zhou,R.L., Arias L.A.C., Shendelman,J.M., Zazubovits,N., Borsuk,L.A., Emrich,S.J., Ashlock,D.A., Scanlon,M.J. and Schnable,P.S.
Expressed Sequence Tags from B73 Maize Shoot Apical Meristems
Unpublished (2004)
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
Tel: 515-294-0975
Fax: 515-294-5256
Email: schnable@iastate.edu.

TITLE
JOURNAL
COMMENT

FEATURES
source

Location/Qualifiers
1..692
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="inbred B73"
/db_xref="taxon:4577"
/tissue_type="vegetative Shoot Apical Meristem (SAM) and leaf primordia staged P1-P4"
/lab_host="XLI-Blue"
/clone_lib="UGA-ZmSAM-X22"
/note="Organ: Shoot apex; Vector: Uni-Zap XR; Site 1: EcoRI; Site 2: XhoI; This library was constructed by Xiaolan Zhang. Vegetative Shoot Apical Meristem (SAM) and leaf primordia staged P1-P4 from 14-17 day after germination seedlings were quickly dissected into dry ice under a light microscope. Total RNA was isolated using Trizol and mRNA was purified with Dynal Oligo-DT25. ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an XhoI oligo-dT primer

QY 121 AATTTGGGGGCTCCCGTATGAGATGCTGCCGGGCAAGCCCTCGGTGTCACCACTCGTTT 180
 |||
 Db 169 AATTTGGGGGCTCCCGTATGAGATGCTGCCGGGCAAGCCCTCGGTGTCACCACTCGTTT 110
 |||
 QY 181 GTGGCGGGGGCGCTGGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAACTGTGTCA 240
 |||
 Db 109 GTGGCGGGGGCGCTGGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAACTGTGTCA 50
 |||
 QY 241 CTTGCAATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCTATATC 289
 |||
 Db 49 CTTGCAATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCTATATC 1

RESULT 4
 BE639295/c
 LOCUS BE639295 448 bp mRNA linear EST 30-AUG-2000
 DEFINITION 946020502.y2 946 - tassels primordium prepared by Schmidt lab Zea
 mays cDNA, mRNA sequence.

ACCESSION BE639295
 VERSION BE639295.1 GI:9952607
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 448)

REFERENCE Walbot.V.
 Maize ESTs from various cDNA libraries sequenced at Stanford

AUTHORS Walbot V.
 TITLE University
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 946020 row: E column: 02.

FEATURES
 source
 1..448
 Location/Qualifiers
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="OH43"
 /db_xref="taxon:4577"
 /tissue_type="tassels"
 /dev_stage="just after the transition from vegetative to
 inflorescence development"
 /lab_host="XLOLR"
 /clone_lib="946 - tassels primordium prepared by Schmidt
 lab"
 /note="Organ: tassels; Vector: HybriZAP; Site 1: EcoRI;
 Site 2: XhoI; George Chuck dissected immature tassels
 between 1mm and 3mm. Sharon Stanfield prepared the cDNA
 library in HybriZAP. Sample insert size range was 350 bp
 to 3 Kb with a 1 Kb average."

ORIGIN
 Query Match 97.8%; Score 284.6; DB 2; Length 448;
 Best Local Similarity 98.6%; Pred. No. 3e-76;
 Matches 287; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGCCGGCTTTATGTGCGTGAAGAACTAGTAGCTAGTGTGCTGCTGCGAATGACACTAT 60
 |||
 Db 321 AGCCGGCTTTATGTGCGTGAAGAACTAGTAGCTAGTGTGCTGCTGCGAATGACACTAT 262
 |||
 QY 61 GCAATGTGATCTGGAACTGGTTTCTTGGGTGGCGAGCTAGTTATGACTGTCGTCAGTAA 120
 |||
 Db 261 GCAATGTGATCTGGAACTGGTTTCTTGGGTGGCGAGCTAGTTATGACTGTCGTCAGTAA 202
 |||
 QY 121 AATTTGGGGGCTCCCGTATGAGATGCTGCCGGGCAAGCCCTCGGTGTCACCACTCGTTT 180
 |||

Db 201 AATTTGGGGGCTCCCGTATGAGATGCTGCCGGGCAAGCCCTCGGTGTCACCACTCGTTT 142
 |||
 QY 181 GTGGCGGGGGCGCTGGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAACTGTGTCA 240
 |||
 Db 141 GTGGCGGGGGCGCTGGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAACTGTGTCA 82
 |||
 QY 241 CTTGCAATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCTATATCAA 291
 |||
 Db 81 CTTGCAATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCTATATCAA 31

RESULT 5
 CF061011/c
 LOCUS OQT16d11.y9 OQT Zea mays cDNA clone QCT16d11, mRNA sequence.

ACCESSION CF061011
 VERSION CF061011.1 GI:33101051
 KEYWORDS EST.

SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 404)

REFERENCE Genoplatte.
 AUTHORS Genoplatte, a major partnership french program in plant genomics
 TITLE Unpublished (2003)
 JOURNAL Contact: Genoplatte
 COMMENT

Genoplatte
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>
 and <http://genoplatte-info.infobiogen.fr>).

FEATURES
 source
 1..404
 Location/Qualifiers
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="f333 or f334"
 /db_xref="taxon:4577"
 /clone="OQT16d11"
 /tissue_type="seedling minus kernel"
 /clone_lib="OQT"

ORIGIN
 Query Match 97.1%; Score 282.6; DB 6; Length 404;
 Best Local Similarity 98.6%; Pred. No. 1.2e-75;
 Matches 285; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGCCGGCTTTATGTGCGTGAAGAACTAGTAGCTAGTGTGCTGCTGCGAATGACACTAT 60
 |||
 Db 290 AGCCGGCTTTATGTGCGTGAAGAACTAGTAGCTAGTGTGCTGCTGCGAATGACACTAT 231
 |||
 QY 61 GCAATGTGATCTGGAACTGGTTTCTTGGGTGGCGAGCTAGTTATGACTGTCGTCAGTAA 120
 |||
 Db 230 GCAATGTGATCTGGAACTGGTTTCTTGGGTGGCGAGCTAGTTATGACTGTCGTCAGTAA 171
 |||
 QY 121 AATTTGGGGGCTCCCGTATGAGATGCTGCCGGGCAAGCCCTCGGTGTCACCACTCGTTT 180
 |||
 Db 170 AATTTGGGGGCTCCCGTATGAGATGCTGCCGGGCAAGCCCTCGGTGTCACCACTCGTTT 111
 |||
 QY 181 GTGGCGGGGGCGCTGGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAACTGTGTCA 240
 |||
 Db 110 GTGGCGGGGGCGCTGGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAACTGTGTCA 51
 |||
 QY 241 CTTGCAATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCTATATC 289
 |||
 Db 50 CTTGCAATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCTATATC 2

RESULT 6
 CF061154/c

LOCUS CF061154 437 bp mRNA linear EST 21-JUL-2003
 DEFINITION OCT18c03.yg QCT Zea mays cDNA clone QCT18c03, mRNA sequence.
 ACCESSION CF061154
 VERSION CF061154.1 GI:33101194

KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 437)

AUTHORS Genoplante.
 TITLE Genoplante, a major partnership french program in plant genomics
 JOURNAL Unpublished (2003)

COMMENT Contact: Genoplante

Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>
 and <http://genoplante-info.infobiogen.fr>).

FEATURES

Location/Qualifiers
 1..437
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="F333 or f334"
 /db_xref="taxon:4577"
 /clone="QCT18c03"
 /tissue_type="seedling minus kernel"
 /clone_lib="QCT"

ORIGIN

Query Match 96.6%; Score 281; DB 6; Length 437;
 Best Local Similarity 98.3%; Pred. No. 3.8e-75;
 Matches 284; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 ACCCGCTTTATGCGGTAGAACTAGTAGCTAGTGTGCTGCTGCTGCAATGACACTAT 60
 DB 289 AGCCGGCTTTATGCGGTAGAACTAGTAGCTAGTGTGCTGCTGCTGCAATGACACTAT 230
 QY 61 GCAATGTGATCTGGAACCTGTTCTTGGGTGCGAGCTAGTTATGACTGTGTCAGTAA 120
 DB 229 GCAATGTGATCTGGAACCTGTTCTTGGGTGCGAGCTAGTTATGACTGTGTCAGTAA 170
 QY 121 AATTGGGGGCTCCCGTATGAGATGCTCCGGGCAAGCCCTCGGTGTCACCTCGTTT 180
 DB 169 AATTGGGGGCTCCCGTATGAGATGCTCCGGGCAAGCCCTCGGTGTCACCTCGTTT 110
 QY 181 GTGGCGGGGGCGCTGGAGCCCGGTCTGTTGGTTGGGAAGCCCTTTAAACTGTTGTCA 240
 DB 109 GTGGCGGGGGCGCTGGAGCCCGGTCTGTTGGTTGGGAAGCCCTTTAAACTGTTGTCA 50
 QY 241 CTTCGATTTTACCTTTTCCATCGCTGTTTATGAGTGGTCTCTATATC 289
 DB 49 CTTCGATTTTACCTTTTCCATCGCTGTTTATGAGTGGTCTCTATATC 1

RESULT 7
 BM888666/c

LOCUS BM888666 313 bp mRNA linear EST 08-MAR-2002
 DEFINITION 952067E09.y1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea
 mays cDNA, mRNA sequence.

ACCESSION BM888666
 VERSION BM888666.1 GI:19772410

KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 313)

AUTHORS Walbot,V.

Maize ESTs from various cDNA libraries sequenced at Stanford
 University
 Unpublished (1999)
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 952067 row: E column: 09.

FEATURES

Location/Qualifiers
 1..313
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="BMS (Black Mexican Sweet)"
 /db_xref="taxon:4577"
 /tissue_type="suspension culture"
 /dev_stage="mixed logarithmic and stationary growth
 phases"
 /lab_host="DH10B"
 /clone_lib="952 - BMS tissue from Walbot Lab (reduced
 rRNA)"
 /note="Vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; The
 library was prepared by George Rudenko using poly (A)
 selected RNA and Universal Riboclone cDNA Synthesis System
 (Promega). cDNA was synthesized using both random and
 oligo(dT) primers in separate reactions and equipped with
 EcoRI adaptors. Library was size-fractionated on agarose
 gels (for insert size >400bp) and non-directionally cloned
 into EcoRI-digested pUC19 vector. Blue/white selection on
 carbenicillin-containing plates was used to recover
 positive clones."

ORIGIN

Query Match 96.2%; Score 279.8; DB 3; Length 313;
 Best Local Similarity 97.6%; Pred. No. 8.3e-75;
 Matches 284; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 AGCCGGCTTTATGCGGTAGAACTAGTAGCTAGTGTGCTGCTGCAATGACACTAT 60
 DB 293 AGCCGGCTTTATGCGGTAGAACTAGTAGCTAGTGTGCTGCTGCAATGACACTAT 234
 QY 61 GCAATGTGATCTGGAACCTGTTCTTGGGTGCGAGCTAGTTATGACTGTGTCAGTAA 120
 DB 233 GCAATGTGATCTGGAACCTGTTCTTGGGTGCGAGCTAGTTATGACTGTGTCAGTAA 174
 QY 121 AATTGGGGGCTCCCGTATGAGATGCTCCGGGCAAGCCCTCGGTGTCACCTCGTTT 180
 DB 173 AATTGGGGGCTCCCGTATGAGATGCTCCGGGCAAGCCCTCGGTGTCACCTCGTTT 114
 QY 181 GTGGCGGGGGCGCTGGAGCCCGGTCTGGTTGGTTGGGAAGCCCTTTAAACTGTTGTCA 240
 DB 113 GTGGCGGGGGCGCTGGAGCCCGGTCTGGTTGGTTGGGAAGCCCTTTAAACTGTTGTCA 54
 QY 241 CTTCGATTTTACCTTTTCCATCGCTGTTTATGAGTGGTCTCTATATCA 291
 DB 53 CTTCGATTTTACCTTTTCCATCGCTGTTTATGAGTGGTCTCTATATCA 3

RESULT 8

BM895191/c

LOCUS BM895191 313 bp mRNA linear EST 11-MAR-2002
 DEFINITION 952066H10.y1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea
 mays cDNA, mRNA sequence.

ACCESSION BM895191
 VERSION BM895191.1 GI:19350659

KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 313)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 952066 row: H column: 10.

FEATURES
source

1..313
Location/Qualifiers
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="BMS (Black Mexican Sweet)"
/db_xref="taxon:4577"
/tissue_type="suspension culture"
/dev_stage="mixed logarithmic and stationary growth phases"
/lab_host="DH10B"
/clone_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)"
/note="Vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; The library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicillin-containing plates was used to recover positive clones."

ORIGIN

Query Match 96.2%; Score 279.8; DB 3; Length 313;
Best Local Similarity 97.6%; Pred. No. 8.3e-75;
Matches 284; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AGCCGGCTTTATGCGTAGAACTAGTAGCTAGTGTGCTGCTGCGAATGACACTAT 60
DB 293 AGCCGGCTTTATGCGTAGAACTAGTAGCTAGTGTGCTGCTGCGAATGACACTAT 234
QY 61 GCAATGTGATCTGGAACCTGGTTCTTGGGTGCGACGCTAGTATGACTGTCGTCAGTAA 120
DB 233 GCAATGTGATCTGGAACCTGGTTCTTGGGTGCGACGCTTGTATGACTGTCATCGGTAA 174
QY 121 AATTTGGGGGCTCCCGTATGAGATGCTGCGGCGAAGCCCTGCGTGCCACCTCGTTT 180
DB 173 AATTTGGGGGCTCCCGTATGAGATGCTGCGGCGAAGCCCTGCGTGCCACCTCGTTT 114
QY 181 GTGGGGGGGGCGCTGGAGCCCGGTCTGTTGGGTTGGGAAGCCCTTTAAACTGTGTGCA 240
DB 113 GTGGGGGGGGCGCTGGAGCCCGGTCTGTTGGGTTGGGAAGCCCTTTAAACTGTGTGCA 54
QY 241 CTTCATTTTACCTTTTCATCGCTGTTTATGAGTGCTCTATATCA 291
DB 53 CTTCATTTTACCTTTTCATCGCTGTTTATGAGTGCTCTATATCA 3

RESULT 9
AI738207/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AI738207
606047B11.x1 606 - Ear tissue cDNA library from Schmidt lab Zea mays cDNA, mRNA sequence.
AI738207
AI738207.1 GI:5081161
EST.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 599)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 606047 row: B column: 11.

FEATURES
source

1..599
Location/Qualifiers
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="Ohio43"
/db_xref="taxon:4577"
/tissue_type="mixed"
/dev_stage="ear length from 0.5 cm - 2.0 cm"
/lab_host="XLOLR (Stratagene)"
/clone_lib="606 - Ear tissue cDNA library from Schmidt lab"
/note="Organ: immature ear; Vector: pBK-CMV; Site 1: EcoRI; Site 2: XhoI; Mixed ear tissue cDNA library from Schmidt lab"

ORIGIN

Query Match 96.2%; Score 279.8; DB 1; Length 599;
Best Local Similarity 97.6%; Pred. No. 9.5e-75;
Matches 284; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AGCCGGCTTTATGCGTAGAACTAGTAGCTAGTGTGCTGCTGCGAATGACACTAT 60
DB 305 AGCCGGCTTTATGCGTAGAACTAGTAGCTAGTGTGCTGCTGCGAATGACACTAT 246
QY 61 GCAATGTGATCTGGAACCTGGTTCTTGGGTGCGACGCTAGTATGACTGTCGTCAGTAA 120
DB 245 GCAATGTGATCTGGAACCTGGTTCTTGGGTGCGACGCTTGTATGACTGTCATCGGTAA 186
QY 121 AATTTGGGGGCTCCCGTATGAGATGCTGCGGCGAAGCCCTGCGTGCCACCTCGTTT 180
DB 185 AATTTGGGGGCTCCCGTATGAGATGCTGCGGCGAAGCCCTGCGTGCCACCTCGTTT 126
QY 181 GTGGGGGGGGCGCTGGAGCCCGGTCTGTTGGGTTGGGAAGCCCTTTAAACTGTGTGCA 240
DB 125 GTGGGGGGGGCGCTGGAGCCCGGTCTGTTGGGTTGGGAAGCCCTTTAAACTGTGTGCA 66
QY 241 CTTCATTTTACCTTTTCATCGCTGTTTATGAGTGCTCTATATCA 291
DB 65 CTTCATTTTACCTTTTCATCGCTGTTTATGAGTGCTCTATATCA 15

RESULT 10
AW061962/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AW061962
687009G02.x1 687 - Early embryo from Delaware Zea mays cDNA, mRNA sequence.
AW061962
AW061962.1 GI:6012525
EST.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 628)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford University

JOURNAL
COMMENT

Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 687009 row: G column: 02.
Location/Qualifiers

FEATURES
source

1. .628
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="Illinois High Oil"
/db_xref="taxon:4577"
/issue_type="embryo"
/dev_stage="14, 21, 28, and 35 days after pollination"
/lab_host="E. coli SOLR"
/clone_lib="687 - Early embryo from Delaware"
/note="Organ: embryo; Vector: pBluescript SK; Site: 1: XhoI; Site: 2: EcoRI; Library was prepared by statagene using the Uni-ZAP XR system (Stratagene BN937328-12). Clones were picked by a Q-bot after blue/white selection (ampicillin resistance - use 100 micrograms/microliter). Developed from a pool of equal amounts of RNA from developing embryos sampled at 14, 21, 28 and 35 days after pollination of the Illinois High Oil Maize Strain Cycle 90. This closed strain has been selected for high oil concentration for 90 generations and originates from the 1890s era open pollinated variety Burr's White"

ORIGIN

Query Match 95.6%; Score 278.2; DB 1; Length 628;
Best Local Similarity 97.3%; Pred. No. 3e-74;
Matches 283; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 AGCCGGCTTATGCGTAGAAGCTAGTAGCTAGTTGCTGCTGCGAATGACACTAT 60
DB 310 AGCCGGCTTATGCGTAGAAGCTAGTAGCTAGTTGCTGCTGCGAATGACACTAT 251

QY 61 GCAATGTGATCTGGAACCTGTTCTTGGGTGCGAGCTAGTTATGACTGCTCAGTAA 120
DB 250 GCAATGTGATCTGGAACCTGTTCTTGGGTGCGAGCTAGTTATGACTGCTCAGTAA 191

QY 121 AATTGGGGGCTCCCGTATGAGATGCTCCCGGCAAGCCCTCGGTGCCACCTCGTTT 180
DB 190 AATTGGGGGCTCCCGTATGAGATGCTCCCGGCAAGCCCTCGGTGCCACCTCGTTT 131

QY 181 GTGGGGGGGGCGCTGGAGCCGGTCTGTTGGTTGGGAAGCCCTTAAACTGTGTGCA 240
DB 130 GTGGGGGGGGCGCTGGAGCCGGTCTGTTGGTTGGGAAGCCCTTAAACTGTGTGTC 71

QY 241 CTTGCATTTTACCTTTCCATCGCTGTTTATGAGTGGTCTTATATCAA 291
DB 70 CTTGCATTTTACCTTTCCATCGCTGTTTATGAGTGGTGTGCAAAAAA 20

RESULT 11
BQ163609/c
LOCUS BQ163609 290 bp mRNA linear EST 24-APR-2002
DEFINITION 952077G01.y3 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea mays cDNA, mRNA sequence.
ACCESSION BQ163609
VERSION BQ163609.1 GI:20300666
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 290)
AUTHORS Walbot.V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford

JOURNAL
COMMENT

Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 952077 row: G column: 01.
Location/Qualifiers

FEATURES
source

1..290
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="BMS (Black Mexican Sweet)"
/db_xref="taxon:4577"
/issue_type="suspension culture"
/dev_stage="mixed logarithmic and stationary growth phases"
/lab_host="DH10B"
/clone_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)"
/note="Vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; The library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicillin-containing plates was used to recover positive clones."

ORIGIN

Query Match 95.1%; Score 276.8; DB 3; Length 290;
Best Local Similarity 97.6%; Pred. No. 6.8e-74;
Matches 281; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 CGGCTTTATGCGTAGAAGCTAGTAGCTAGTTGCTGCTGCGAATGACACTATGCA 63
DB 290 CGGCTTTATGCGTAGAAGCTAGTAGCTAGTTGCTGCTGCGAATGACACTATGCA 231

QY 64 ATGTGATCTGGAACCTGTTCTTGGGTGCGAGCTAGTTATGACTGCTCAGTAAAT 123
DB 230 ATGTGATCTGGAACCTGTTCTTGGGTGCGAGCTAGTTATGACTGCTCAGTAAAT 171

QY 124 TTGGGGGCTCCCGTATGAGATGCTCCCGGCAAGCCCTCGGTGCCACCTCGTTTGTG 183
DB 170 TTGGGGGCTCCCGTATGAGATGCTCCCGGCAAGCCCTCGGTGCCACCTCGTTTGTG 111

QY 184 CGGGGGGCGCTGGAGCCGGTCTGTTGGTTGGGAAGCCCTTAAACTGTGTGCACTT 243
DB 110 CGGGGGGCGCTGGAGCCGGTCTGTTGGTTGGGAAGCCCTTAAACTGTGTGCACTT 51

QY 244 GCATTTTACCTTTCCATCGCTGTTTATGAGTGGTCTTATATCAA 291
DB 50 GCATTTTACCTTTCCATCGCTGTTTATGAGTGGTGTGCGACACAA 3

RESULT 12
BQ163007/c
LOCUS BQ163007 409 bp mRNA linear EST 24-APR-2002
DEFINITION 952032D09.y2 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea mays cDNA, mRNA sequence.
ACCESSION BQ163007
VERSION BQ163007.1 GI:20300064
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 409)

AUTHORS
TITLE Walbot.V.
JOURNAL Maize ESTs from various cDNA libraries sequenced at Stanford
COMMENT University
 Unpublished (1999)
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 952032 row: D column: 09.

FEATURES

source
 1. 409
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="BMS (Black Mexican Sweet)"
 /db_xref="taxon:4577"
 /tissue_type="suspension culture"
 /dev_stage="mixed logarithmic and stationary growth phases"
 /lab_host="DH108"
 /clone_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)"
 /note="Vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; The library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicillin-containing plates was used to recover positive clones."

ORIGIN

Query Match 95.1%; Score 276.6; DB 3; Length 409;
 Best Local Similarity 98.6%; Pred. No. 8.4e-74;
 Matches 279; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 AGCCGGCTTTATGTCGTAGAAACTAGTAGCTAGTGTGCTGTGCTGCGAATGACACTAT 60
 Db 294 AGCCGGCTTTATGTCGTAGAAACTAGTAGCTAGTGTGCTGTGCTGCGAATGACACTAT 235
 QY 61 GCAATGTGATCTGGAACTGGTTCTTGGTCGAGAGCTAGTATGACTGTGCTCAGTAA 120
 Db 234 GCAATGTGATCTGGAACTGGTTCTTGGTCGAGAGCTAGTATGACTGTGCTCAGTAA 175
 QY 121 AATTTGGGGGCTCCCGGTATGAGATGCTCGCGGCAAGCCCTCGGTGCCACCTCGTTT 180
 Db 174 AATTTGGGGGCTCCCGGTATGAGATGCTCGCGGCAAGCCCTCGGTGCCACCTCGTTT 115
 QY 181 GTGGCGGGGGCGCTGGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAACTGTGTGCA 240
 Db 114 GTGGCGGGGGCGCTGGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAACTGTGTGCA 55
 QY 241 CTTCGATTTTACCTTTCCATCGCTGTTTATGTGAGTGGTCC 283
 Db 54 CTTCGATTTTACCTTTCCATCGCTGTTTATGTGAGTGGTCC 12

RESULT 13
 AW519844
 LOCUS 660053H10.Y1 660 - Mixed stages of anther and pollen Zea mays cDNA, mRNA sequence.
 DEFINITION
 ACCESSION AW519844
 VERSION AW519844.1 GI:7162237
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

REFERENCE

AUTHORS
TITLE Walbot.V.
JOURNAL Maize ESTs from various cDNA libraries sequenced at Stanford
COMMENT University
 Unpublished (1999)
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 660053 row: H column: 10.

FEATURES

source
 1. 461
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="Ohio43"
 /db_xref="taxon:4577"
 /tissue_type="whole premeiotic anthers to pollen shed"
 /dev_stage="premeiotic anthers to pollen shed"
 /lab_host="XLOR"
 /clone_lib="660 - Mixed stages of anther and pollen"
 /note="Organ: anthers; Vector: Lambda Zap; Site 1: EcoRI; Site 2: XhoI; Anther and pollen cDNA library. Directionally sequenced with 5' end at the EcoRI site. Created by Amie Franklin."

ORIGIN

Query Match 95.1%; Score 276.6; DB 1; Length 461;
 Best Local Similarity 96.9%; Pred. No. 8.6e-74;
 Matches 282; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 AGCCGGCTTTATGTCGTAGAAACTAGTAGCTAGTGTGCTGTGCTGCGAATGACACTAT 60
 Db 159 AGCCGGCTTTATGTCGTAGAAACTAGTAGCTAGTGTGCTGTGCTGCGAATGACACTAT 218
 QY 61 GCAATGTGATCTGGAACTGGTTCTTGGTCGACGCTAGTATGACTGTGCTCAGTAA 120
 Db 219 GCAATGTGATCTGGAACTGGTTCTTGGTCGACGCTTGTATGACTGTGCTCAGTAA 278
 QY 121 AATTTGGGGGCTCCCGGTATGAGATGCTCGCGGCAAGCCCTCGGTGCCACCTCGTTT 180
 Db 279 AATTTGGGGGCTCCCGGTATGAGATGCTCGCGGCAAGCCCTCGGTGCCACCTCGTTT 338
 QY 181 GTGGCGGGGGCGCTGGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAACTGTGTGCA 240
 Db 339 GTGGCGGGGGCGCTGGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAACTGTGTGCA 398
 QY 241 CTTCGATTTTACCTTTCCATCGCTGTTTATGTGAGTGGTCCATATCAA 291
 Db 399 CTTCGATTTTACCTTTCCATCGCTGTTTATGTGAGTGGTCCCAAAAAA 449

RESULT 14

DN217785
 LOCUS 289 bp mRNA linear EST 28-FEB-2005
 DEFINITION MEST800 E04.T7-1 UGA-ZmSAM-X22 Zea mays cDNA, mRNA sequence.
 ACCESSION DN217785
 VERSION DN217785.1 GI:60350812
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 289)
 Chen, H.D., Zhang, X., Zhou, R.L., Arias, L.A.C., Shendelman, J.M., Zazubovits, N., Borsuk, L.A., Enrich, S.J., Ashlock, D.A., Scanlon, M.J. and Schnable, P.S.
 Expressed Sequence Tags from B73 Maize Shoot Apical Meristems
 Unpublished (2004)


```
QY 1 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGCTGTGTCGAAATGACACTAT 60
Db |||||||
QY 14 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGCTGTGTCGAAATGACACTAT 73
Db |||||||
QY 61 GCAATGTGATCTGGAACTGGTTCTTGGGTGCGACGCTAGTATGACTGTGTCAGTAA 120
Db |||||||
QY 74 GCAATGTGATCTGGAACTGGTTCTTGGGTGCGACGCTTGTATGACTGTGTCAGTAA 133
Db |||||||
QY 121 AATTTGGGGGCTCCCGGTATGAGATGCTGCCGGGCAAGGCTTCGGTGTCGCCACCTCGTTT 180
Db |||||||
QY 134 AATTTGGGGGCTCCCGGTATGAGATGCTGCCGGGCAAGGCTTCGGTGTCGCCACCTCGTTT 193
Db |||||||
QY 181 GTGGCGGGGGCGCTGGAGCCCGTCTGGTTGGGTTGGGAGCCCTTTAAACTGTGTCA 240
Db |||||||
QY 194 GTGGCGGGGGCGCTGGAGCCCGTCTGGTTGGGTTGGGAGCCCTTTAAACTGTGTCA 253
Db |||||||
QY 241 CTTGCATTTTACCTTTTCATCGCTGTTTATTGTGAG 277
Db |||||||
QY 254 CTTGCATTTTACCTTTTCATCGCTGTTTATTGTGAG 290
Db |||||||
```

Search completed: March 8, 2006, 05:42:27
Job time : 2340.81 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 23:00:44 ; Search time 122.379 Seconds
(without alignments)
4226.797 Million cell updates/sec

Title: US-10-603-524A-2

Perfect score: 291

Sequence: 1 agccggctttatgtcgtag.....tgtgagtggtctatatcaa 291

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/1 COMB.seq:*
- 2: /cgn2_6/prodata/1/ina/5 COMB.seq:*
- 3: /cgn2_6/prodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/prodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/prodata/1/ina/H COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/PCUS COMB.seq:*
- 7: /cgn2_6/prodata/1/ina/PP COMB.seq:*
- 8: /cgn2_6/prodata/1/ina/RE COMB.seq:*
- 9: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	34.6	11.9	1469	3	US-09-949-016-5398
C 2	34.6	11.9	75378	3	US-09-949-016-17140
C 3	33.2	11.4	12787	3	US-09-949-016-16359
C 4	32.4	11.1	516	3	US-09-252-991A-16362
C 5	32.4	11.1	846	3	US-09-252-991A-16471
C 6	32.4	11.1	885	3	US-09-252-991A-16130
C 7	31.8	10.9	103377	3	US-09-949-016-14089
C 8	30.8	10.6	601	3	US-09-949-016-177958
C 9	30.8	10.6	7381	3	US-09-949-016-16844
C 10	30.4	10.4	25230	3	US-09-949-016-13153
C 11	30.2	10.4	435	3	US-09-134-001C-2640
C 12	30.2	10.4	505	3	US-09-621-976-15639
C 13	30.2	10.4	601	3	US-09-949-016-27361
C 14	30.2	10.4	601	3	US-09-949-016-149636
C 15	30.2	10.4	901	3	US-09-311-021-91
C 16	30.2	10.4	3798	3	US-09-949-016-4204
C 17	30.2	10.4	3839	3	US-09-949-016-485
C 18	30.2	10.4	156942	3	US-09-949-016-12227
C 19	30.2	10.4	156950	3	US-09-949-016-15946
C 20	30	10.3	1023	3	US-09-489-039A-5154
C 21	30	10.3	2067	3	US-09-106-194-11
C 22	29.8	10.2	601	3	US-09-949-016-150193
C 23	29.8	10.2	1158	3	US-09-902-540-6363
C 24	29.8	10.2	3109	3	US-09-902-540-413

C 25	29.8	10.2	90618	3	US-09-949-016-15964	Sequence 15964, A
C 26	29.6	10.2	858	3	US-09-252-991A-13905	Sequence 13905, A
C 27	29.6	10.2	1062	3	US-08-611-757-33	Sequence 33, Appl
C 28	29.6	10.2	1062	6	PCT-US95-05980-33	Sequence 33, Appl
C 29	29.6	10.2	1461	3	US-09-252-991A-13798	Sequence 13798, A
C 30	29.6	10.2	1656	3	US-09-252-991A-13545	Sequence 13545, A
C 31	29.6	10.2	8256	3	US-09-949-016-16951	Sequence 16951, A
C 32	29.6	10.2	80269	3	US-09-949-016-15681	Sequence 15681, A
C 33	29.4	10.1	1633	3	US-09-023-655-124	Sequence 124, App
C 34	29.4	10.1	57320	3	US-09-949-016-13983	Sequence 13983, A
C 35	29.2	10.0	474	3	US-09-621-976-18033	Sequence 18033, A
C 36	29.2	10.0	56302	3	US-09-949-016-11892	Sequence 11892, A
C 37	29	10.0	1391	3	US-09-270-767-13275	Sequence 13275, A
C 38	29	10.0	13164	3	US-09-949-016-11759	Sequence 11759, A
C 39	29	10.0	15165	3	US-09-949-016-15664	Sequence 15664, A
C 40	29	10.0	100463	3	US-09-949-016-12511	Sequence 12511, A
C 41	29	10.0	100468	3	US-09-949-016-13725	Sequence 13725, A
C 42	28.8	9.9	601	3	US-09-949-016-20694	Sequence 20694, A
C 43	28.8	9.9	1449	3	US-09-088-425-4	Sequence 4, Appl
C 44	28.8	9.9	1449	3	US-09-639-378A-4	Sequence 4, Appl
C 45	28.8	9.9	1762	3	US-09-799-451-622	Sequence 622, App

ALIGNMENTS

RESULT 1

US-09-949-016-5398/c
; Sequence 5398, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5398
; LENGTH: 1469
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-5398

Query Match 11.9%; Score 34.6; DB 3; Length 1469;
Best Local Similarity 55.4%; Pred. No. 0.15;
Matches 67; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY	93	CGACGCTAGTTATGACTGCTCGTCAGTAAATTTGGGGGCTCCCCGTATGAGATGCTGCGG	152
DB	151	CAAGGCCACTCATGGCATTGCTCTCGAGGCTGGGGGCTCTCCAGGAGGATGATGACC	92
QY	153	GGCAAGGCTCGTGTGTCACCTCGTTTGTGGGGGGGGCGCTGAGCCCGGCTTGTTG	212
DB	91	GTGGCCCCCTGAAGACGCCCTGGCCCTCTCGAGGGGCGATGCTGAGCTGCGACTGTTG	32
QY	213	G 213	
DB	31	G 31	

RESULT 2

US-09-949-016-17140/c
; Sequence 17140, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

```
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17140
; LENGTH: 75378
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(75378)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17140

Query Match          11.9%; Score 34.6; DB 3; Length 75378;
Best Local Similarity 55.4%; Pred. No. 1.2;
Matches 67; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

Qy 93 CGACCTAGTTATGACTGTCGTCAGTAAATTTGGGGGCTCCCCGTATGAGATGCTGCCG 152
Db 2151 CAAGGCCACTCATGCAATTTGCTCTGAGGCTGGGGGCTCTCCAGGGAGATGATGACC 2092

Qy 153 GCAGAGGCTCGGTCTCCACCTCTGTTGGCGGGGGCGTGAGACCCGTCGTGTTG 212
Db 2091 GTGGCCCTCTGAAGACGCCCTGCGCCCTCTGAGGGGCATGCTGAGCTGCGACTGTGG 2032

Qy 213 G 213
Db 2031 G 2031

RESULT 3
US-09-949-016-16359
; Sequence 16359, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16359
; LENGTH: 12787
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16359

Query Match          11.4%; Score 33.2; DB 3; Length 12787;
Best Local Similarity 52.1%; Pred. No. 1.5;
Matches 74; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 128 GGGCTCCCGTATGAGATGCTCCCGCAAGCCCTCGGTGTCCACCTCGTTTGGCGGG 187
Db 7738 GGGCACCTCTGTCAGAGACTCGAGAGAGGCTACCTGGGCTACTACCTCCAGGGTAG 7797
```

```
Qy 188 GGGGCGCTGGAGCCCGGCTGCTGGTTGGTTGGAGCCCTTTAAACTGTTGTCACTTGCAAT 247
Db 7798 GTGCGCGGGGGCCCTCTCTCCAGGGGGTTCCGGATTCTATTGACCTTAGCCGCCCCAC 7857

Qy 248 TTTACCTTTTCCATCGCTGTTT 269
Db 7858 TTCTTTTCTTAAGCGAGTT 7879

RESULT 4
US-09-252-991A-16362
; Sequence 16362, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16362
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16362

Query Match          11.1%; Score 32.4; DB 3; Length 516;
Best Local Similarity 53.1%; Pred. No. 0.51;
Matches 69; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 77 CCTGGTTTCTTGGGTGGCGAGCTAGTTATGACTGTCGTCAGTAAATTTGGGGGCTCCCC 136
Db 91 CCTGGGCTCTTGGCGCGCGCTGCTGCTGCTGGACAGACCTGCTTGTGCGGCCAC 150

Qy 137 GTATGAGATGCTGCCGGGCAAGGCTCGGTGTCCACCTCGTTTGTGCGGGGGCGCTG 196
Db 151 CCTGGCCCGCTGCTGGCCCTGGCGGCGATGGCGGCTGAGGGTTTCGCGGTCG 210

Qy 197 GAGCCCGGTC 206
Db 211 GGGAGAGGCG 220

RESULT 5
US-09-252-991A-16471
; Sequence 16471, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16471
; LENGTH: 846
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16471

Query Match          11.1%; Score 32.4; DB 3; Length 846;
Best Local Similarity 53.1%; Pred. No. 0.66;
```


Matches 69; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
QY 77 CTGTTTCTGGTGGCGAGCGTAGTATGATGTCAGTAAATTTGGGGCTCCCC 136
Db 303 CCTGGGCTCTGGCGGGCGCTGCTCTCCCTGAGCAAGACCCCTGTTGGTCGCCAC 362
QY 137 GTATGAGATGCTGCCGGCAAGCCCTCGGTGTCACACCTGTTTGGCGGGGGCGCTG 196
Db 363 CCTGGCCGCTGCTGGCCCTGGCGCGATGGCGCCCTGGAGGGTTCCCGGTTGGCGCG 422
QY 197 GAGCCCGGTC 206
Db 423 GCGAGAGGCG 432

RESULT 6
US-09-252-991A-16130/c
; Sequence 16130, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16130
; LENGTH: 885
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16130

Query Match 11.1%; Score 32.4; DB 3; Length 885;
Best Local Similarity 53.1%; Pred. No. 0.68;
Matches 69; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
QY 77 CTGTTTCTGGTGGCGAGCGTAGTATGATGTCAGTAAATTTGGGGCTCCCC 136
Db 487 CTGGGCTCTGGCGGGCGCTGGCTCTGCCCTGAGCAAGACCCCTGCTGGTCGCCAC 428
QY 137 GTATGAGATGCTGCCGGCAAGCCCTCGGTGTCACACCTGTTTGGCGGGGGCGCTG 196
Db 427 CCTGGCCGCTGCTGGCCCTGGCGCGATGGCGCCCTGGAGGGTTCCCGGTTGGCGCG 368
QY 197 GAGCCCGGTC 206
Db 367 GCGAGAGGCG 358

RESULT 7
US-09-949-016-14089
; Sequence 14089, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14089
; LENGTH: 103377
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(103377)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14089

Query Match 10.9%; Score 31.8; DB 3; Length 103377;
Best Local Similarity 59.3%; Pred. No. 14;
Matches 54; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
QY 12 TGTGCGTAGAACTAGTAGTGTGTTGCTGCTCGAATGACACTATGCAATGTGATC 71
Db 73138 TGTGCTAAATGTCAAAAGTTGTGTTGTGCTGTGAAGGCCACTTTGCAATGCTCCC 73197
QY 72 TCGAACCTGGTTCTTGTGGTGGCGAGCGTAGT 102
Db 73198 TAGAACTTGGGTATGTGGCGAGGAGATGGT 73228

RESULT 8
US-09-949-016-177958/c
; Sequence 177958, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177958
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-177958

Query Match 10.6%; Score 30.8; DB 3; Length 601;
Best Local Similarity 54.4%; Pred. No. 2;
Matches 62; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
QY 125 TGGGGGCTCCCGTATGAGATGTCGCCGGGCAAGCCCTCGGTGTCACCTCGCTTTGTGG 184
Db 482 TGGGGGTAGCAGGTTTGAGATGCTGTCGGGTGTCGGGTCCAGGCCAGCTAGGCTCAGC 423
QY 185 CGGGGGCGCTGGAGCCCGGCTGTTGGTGGGAAGCCCTTTAAACTGTTGT 238
Db 422 TGTGGAGGAGAACGCTGCGGCCCGGGGCGCTGCGGTGTCCTGAAGCTCCTGT 369

RESULT 9
US-09-949-016-16844
; Sequence 16844, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

```
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16844
; LENGTH: 7381
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; LOCATION: (1)_(7381)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16844

Query Match          10.6%; Score 30.8; DB 3; Length 7381;
Best Local Similarity 54.4%; Pred. No. 7.6;
Matches 62; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 125 TGGGGCTCCCGTATGAGTGTCCCGGCAAGCCCTCGGTGCCACCTGTTTGGG 184
      |||||
Db 3731 TGGGGTAGCAGGTTTGAGATGCTGCGGTGCTGGGTCCAGGCCAGGCTAGGCTCAGC 3790

Qy 185 CGGGGGCGCTGGAGCCCGTCTGTTGGTTGGGAAGCCCTTTAAACTGTTGT 238
      |||||
Db 3791 TGTGGGAGGAGAACGCTGGCCCGGAGGCGCTGGGTGTCCCTGAAGCTCCTGT 3844

RESULT 10
US-09-949-016-13153
; Sequence 13153, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13153
; LENGTH: 25230
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13153

Query Match          10.4%; Score 30.4; DB 3; Length 25230;
Best Local Similarity 63.9%; Pred. No. 20;
Matches 46; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 69 ATCTGGAACCTGTTTCTTTGGGTGCGAGCCTAGTTATGACTGCTCAGTAAATTTGGG 128
      |||||
Db 13804 ATATACATCTCTGGTTGCTGGGGGATACCACTTTATGCTGTGCTCAGGCATAATTAAC 13863

Qy 129 GGCTCCCCGTAT 140
      |||||
Db 13864 AGCACCCCTTTT 13875

RESULT 11
US-09-134-001C-2640/c
; Sequence 2640, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
```

```
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2640
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2640

Query Match          10.4%; Score 30.2; DB 3; Length 435;
Best Local Similarity 69.5%; Pred. No. 2.7;
Matches 41; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 209 GTTGGTTGGGAAGCCCTTTAAACTGTGTGTCACCTGTCATTTTACCTTTCCATCGCTGT 267
      |||||
Db 192 GTTAGGGGTGCAACATCGATAGACTTTTATCCATTCTTTTACCTTTTCCATATCTGT 134

RESULT 12
US-09-621-976-15639
; Sequence 15639, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15639
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-15639

Query Match          10.4%; Score 30.2; DB 3; Length 505;
Best Local Similarity 11.2%; Pred. No. 3;
Matches 28; Conservative 121; Mismatches 99; Indels 1; Gaps 1;

Qy 22 AACTAGTAGTAGTGTGTTGCTGCTGTCGATGACACTATGCAATGTGATCTGGAACCTGG 81
      |:::|
Db 1 AMAYMSSRYRTSSKSKRYGKYSMYSRWSMKYYAWGREGKYGTSGRCGRGSMCKSWG 60

Qy 82 TTCTCTGGTGGCAGCGCTAGTTATGACTGTCTCAGTAAATTTGGGGGCTCCCGGTATG 141
      |:::|
Db 61 YRYSTMGYKWSKSKMKYSGKMGTSKSTRTKRYTYSKCRKTCTCKRGWSWKRWKWR 120

Qy 142 AGATGC-TGCCGGCAAGCCCTCGGTGTCCCACTCTGTTTGTGGCGGGGGCGCTGGAGC 200
      |:::|
Db 121 RKMYRMYKYSKASYSYRRCRYKRYGTGRTGKRMCKSSRYMYTRYMYKMTGA 180

Qy 201 CCGGTCTGTTGGGTGGGAAGCCCTTAAACTGTGTGTCACCTGTCATTTTACCTTTTCCA 260
      |:::|
Db 181 CYGSKGMSCKGRSKYGSWKWYTGKTYTCTSKYKSKMSYKSKSMCYTYMMCYTYWMC 240

Qy 261 TCGCTGTTT 269
      |||
Db 241 TCTYKSY 249

RESULT 13
US-09-949-016-27361
```

```

; Sequence 27361, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 27361
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-27361

```

	Query Match	10.4%;	Score 30.2;	DB 3;	Length 601;
	Best Local Similarity	62.7%;	Pred. No. 3.3;		
	Matches 47;	Conservative 0;	Mismatches 28;	Indels 0;	Gaps 0;
QY	212	GGGTTGGGAGCCCTTTAAACTGTTGTCACCTTTACCTTTTCATCGCGTGTAT	271		
Db	487	GGGTTGAGAGTCGCTTAAAGTTTTGTCACATCTTTACATTTGTAGGTTTCTCTTCAG	546		
QY	272	TGTGAGTGGTCCCTAT	286		
Db	547	TATGAGTTATCTTAT	561		

RESULT 14
US-09-949-016-149636
; Sequence 149636, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CUG01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 149636
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-149636

	Query Match	10.4%	Score 30.2;	DB 3;	Length 601;
	Best Local Similarity	62.7%;	Pred. No. 3.3;		
	Matches 47;	Conservative 0;	Mismatches 28;	Indels 0;	Gaps 0;
Qy	212	GGGTTGGGAAGCCCTTTAAACTGTTGTCACATTGCAATTTACCTTTCCATCGCGTGTAT	271		
Db	487	GGGTTGAGAGTCGCTAAAGATTTTGTCACATCTTTACATTTGTAGGGTTTCTCTTCAG	546		
Qy	272	TGTGAGTGGTCCTAT	286		
Db	547	TATGAGTTATCTTAT	561		

```

RESULT 15
US-09-311-021-91
; Sequence 91, Application US/09311021
; Patent No. 6706869
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fecht, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6300-11A
; CURRENT APPLICATION NUMBER: US/09/311,021
; CURRENT FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 91
; LENGTH: 901
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-311-021-91

```

	Query Match	Best Local Similarity	50.4%;	Score 30.2;	DB 3;	Length 901;
	Matches 59;	Conservative 0;	Mismatches 48;	Indels 0;	Gaps 0;	
Qy	103	TATGACTGTCGTACATAAATTTGGGGGCTCCCGGATATGATGATGCTCCCGGGGCAAGCCCT	162			
Db	527	TGTCCTCTCAGCAGACAAGTTCAGGTCTCTCTGGCAGAACTGAACAGCGCCAGACCC	586			
Qy	163	CGGTGTCCCACTCGTTTGTGGGGGGGGCGCTGGAGCCCGGTCTGG	209			
Db	587	TGATGAGCTCCCTGGGCTAGAGAGAAAGGTGTCTCAGGCTGTGTGG	633			

Search completed: March 7, 2006, 23:09:18
Job time : 124.379 secs

This Page Blank (uspto)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 04:19:11 : Search time 775.844 Seconds
(without alignments)
865.410 Million cell updates/sec

Title: US-10-603-524A-2
Perfect score: 291
Sequence: 1 agccggctttatgtcgtag.....tgtgagtggtctatatcaa 291

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 7673375 seqs, 1153648444 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:

- 1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
- 2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
- 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
- 4: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
- 5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
- 6: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
- 7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
- 8: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
- 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
- 10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
- 11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
- 12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	183.2	63.0	1252	9	US-11-096-568A-16048
2	33.4	11.5	599	6	US-09-925-065A-16048
3	32.6	11.3	201	12	US-11-124-367A-18466
4	32.6	11.2	553	6	US-09-925-065A-10284
5	32.6	11.2	553	6	US-09-925-065A-10285
6	32.2	11.1	553	6	US-09-925-065A-10286
7	31.4	10.8	656	6	US-09-925-065A-88099
8	31.2	10.7	372	12	US-11-037-243-18
9	30	10.3	566	6	US-09-925-065A-457896
10	30	10.3	629	6	US-09-925-065A-916170
11	30	10.3	634	6	US-09-925-065A-915272
12	30	10.3	100000	12	US-11-124-368A-2913
13	29.8	10.2	630	6	US-09-925-065A-788291
14	29.8	10.2	1149	6	US-09-925-065A-709944
15	29.8	10.2	1785	8	US-10-750-185-50507
16	29.8	10.2	1785	8	US-10-750-623-50507
17	29.6	10.2	7001	12	US-11-011-332A-75
18	29.6	10.2	8252	12	US-11-011-332A-150
19	29.2	10.0	446	6	US-09-925-065A-36828
20	29	10.0	608	6	US-09-925-065A-735119

C 21	29	10.0	608	6	US-09-925-065A-813302	Sequence 813302,
C 22	29	10.0	609	6	US-09-925-065A-842902	Sequence 842902,
C 23	29	10.0	37507	8	US-10-522-037-2	Sequence 2, Appl1
C 24	28.8	9.9	201	12	US-11-124-367A-18466	Sequence 18466, A
C 25	28.8	9.9	168516	12	US-11-121-086-3	Sequence 3, Appl1
C 26	28.6	9.8	312	8	US-10-802-796-361	Sequence 361, Appl
C 27	28.6	9.8	512	6	US-09-925-065A-361224	Sequence 361224,
C 28	28.6	9.8	600	8	US-10-750-185-213	Sequence 213, App
C 29	28.6	9.8	600	8	US-10-750-623-213	Sequence 709945,
C 30	28.6	9.8	1149	8	US-09-925-065A-709945	Sequence 1901, Ap
C 31	28.6	9.8	1419	8	US-10-793-626-1901	Sequence 97, Appl
C 32	28.6	9.8	1510	8	US-10-947-249-97	Sequence 4088, Ap
C 33	28.6	9.8	1968	7	US-10-932-182A-4088	Sequence 4088, Ap
C 34	28.6	9.8	1968	7	US-10-932-182A-4088	Sequence 4088, Ap
C 35	28.6	9.8	2986	8	US-10-793-626-4365	Sequence 4365, Ap
C 36	28.6	9.8	23877	7	US-10-330-773-211	Sequence 211, App
C 37	28.4	9.8	604	6	US-09-925-065A-124990	Sequence 124990,
C 38	28.4	9.8	604	6	US-09-925-065A-124992	Sequence 124992,
C 39	28.4	9.8	604	6	US-09-925-065A-124993	Sequence 124993,
C 40	28.4	9.8	1197	6	US-09-925-065A-40044	Sequence 40044, A
C 41	28.4	9.8	1197	6	US-09-925-065A-40045	Sequence 40045, A
C 42	28.4	9.8	178877	12	US-11-121-086-17	Sequence 17, Appl
C 43	28.2	9.7	598	6	US-09-925-065A-811758	Sequence 811758,
C 44	28.2	9.7	603	6	US-09-925-065A-811760	Sequence 811760,
C 45	28.2	9.7	633	6	US-09-925-065A-848890	Sequence 848890,

ALIGNMENTS

RESULT 1

US-11-096-568A-16048
; Sequence 16048, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 16048
; LENGTH: 1252
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1252)
; OTHER INFORMATION: Ceres Seq. ID no. 12350354
US-11-096-568A-16048

Query Match	63.0%	Score 183.2	DB 9	Length 1252
Best Local Similarity	81.0%	Pred. No. 8.5e-49		
Matches	243	Conservative	0	Mismatches 43; Indels 14; Gaps 2
QY	1	AGCCGGCTTTATGTCGTAGAACTAGTAGTGTGCTGTGCTGCAATGACACTAT	60	
DB	935	AGCCGGCTTTATGTCGTAGAACTAGTAGTGTGCTGTGCTGCTGTGCTGTATGACATTAT	994	
QY	61	GCAATGTGATCTGGAACTGTTTCTTGGTGGCGACGCTAGTATGATGCTGTC-----	112	
DB	995	GCAATGTGATCTGGAACTGTTTCTTGGTGGCGACGCTTGTAGCAGCGCTCTTATGATT	1054	
QY	113	-----GTCACTAAATTTGGGGGCTCCCGTATGATGCTGCGGGCAAGGCTCG--GT	166	
DB	1055	ATTGTGCGGAAATTTGGGGGCTCCCGTATGATGCTGCGGGCAAGGCTCGCCCAT	1114	
QY	167	GTCCCACTCTGTTGTGCGGGGCGCTGAGCGCGGCTGCTGTTGGTGGAGGCGCT	226	
DB	1115	CCCCCACTCTGTTGTGCGGGGCGGCGCTGAGCGCTGCTGCGTTGGTGGAGGCGCT	1174	
QY	227	TAAACTGTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATGTGAGTGGTCTAT	286	

Db 1175 TTAACACTGTTCGCTTGCATTTTAACTTTTCATCGCGTTTCAGTGGTCTTAATCTAT 1234
|||||

RESULT 2

US-09-925-065A-705105/c
; Sequence 705105, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 705105
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-705105

Query Match 11.5%; Score 33.4; DB 6; Length 599;
Best Local Similarity 48.7%; Pred. No. 1;
Matches 91; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 36 GTTCTCTGTCGATGACACTATGCAATGATCTGGAACCTGGTTCTTGGTGCGA 95
Db 526 GGTTCCTGTTGGGGAGGCCCTGGATCTATGCTGTAGAAACATATTCTTCTGTGCC 467
QY 96 CCTAGTTATGATGCTGCTCAGTAAATTTGGGGGCTCCCGTATGAGATGCTGCGGGC 155
Db 466 CTTCACTGAGCCCTTCCAGAGAAATCAGAAAGTCAGGCCCAAGATCTACATGCT 407
QY 156 AAGGCTCGGTTCACCTCTGTTGGCGGGGGCGCTGGAGCCCGTCTGGTTGGGT 215
Db 406 TCTCTCCAGTATCCAACTAATACTAGATTTCAGAGGGGTTGGAGACAGGCAATCCTGGCT 347
QY 216 TGGGAAG 222
Db 346 ACTGAAG 340

RESULT 3

US-11-124-367A-21598
; Sequence 21598, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Honglin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21598
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-21598

Query Match 11.3%; Score 32.8; DB 12; Length 201;
Best Local Similarity 58.5%; Pred. No. 1.1;
Matches 55; Conservative 1; Mismatches 38; Indels 0; Gaps 0;
QY 121 AATTGGGGGCTCCCGTATGAGATGCTGCGGGCAAGGCTCGGTGTCACACCTCGTTT 180
Db 59 AATGAGGCGCTGCCGGAGCCCTCTCTCCACCAATCCCGMGTCTGTCACCCCTGCTT 118
QY 181 GTGGGGGGGGCGCTGGAGCCCGTCTGTTGGG 214
Db 119 GGGGTCTGGGGCTCTGGGGTCTGCTAGGCTGGG 152

RESULT 4

US-09-925-065A-10284/c
; Sequence 10284, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10284
; LENGTH: 553
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-10284

Query Match 11.2%; Score 32.6; DB 6; Length 553;
Best Local Similarity 52.6%; Pred. No. 1.8;
Matches 71; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
QY 3 CCGGCTTTATGTGGGTAGAAACTAGTAGTGTGTTCTGCTGTCGAATGACACTATGC 62
Db 236 CCTACTTTGTAAGCCATAAATCTCTGGGCTCTTAATGATGACCCAGGAGACTCTTC 177
QY 63 AATGATCTCGAACCCTGTTTCTTGGGTGCGAGCGTAGTTATGACTGTCGTCAGTAAA 122
Db 176 AATGACATTTGGATTCTGTTTCTCTGGGAGCTTTCTCTTAATCTGGGATACCTCAA 117
QY 123 TTGGGGGCTCCCG 137
Db 116 GTGTAAGCCAGCCTG 102

RESULT 5

US-09-925-065A-10285/c
; Sequence 10285, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single

RESULT 8
US-11-037-243-18/c
; Sequence 18, Application US/11037243
; Publication NO. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26

Query Match 11.1%; Score 32.2; DB 6; Length 553;
 Pest Local Similarity 51.9%; Pred. No. 2.4;
 Matches 70; Conservative 1; Mismatches 64; Indels 0; Gaps 0

QY - 3 CCGCGTTTATGTGCGTAGAACTAGTACTGTGTTGCTGCTGCGAATGACACTATGC 62

```

; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 3372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-037-243-18

Query Match          10.7%; Score 31.2; DB 12; Length 3372;
Best Local Similarity 57.0%; Pred. No. 9.7;
Matches 57; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 141 GAGATGCTGCCGGGCAAGACCTCGGTGTCCACCTCGTTTGGGGGGGGCGCTGGAGC 200
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 261 GAGCTGGGGCTGGGTCCGGGGGGGGCTTCCTCCCGGGGCTCCCGGGGGCGCTGGAC 202
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 201 CCGGTCTCTGGTGGTGGGAAGCCCTTTAAACTGTTGTCA 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 201 TGGGGCCGGGGGCGAGGCGAAGCCGCCCTCACCGTCGCCA 162

RESULT 9
US-09-925-065A-457896
; Sequence 457896, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 457896
; LENGTH: 566
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-457896

Query Match          10.3%; Score 30; DB 6; Length 566;
Best Local Similarity 57.4%; Pred. No. 13;
Matches 54; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 79 TGGTTCTTGGGTGGGACCTAGTTATGACTGCTGTCAGTAAATTTGGGGGCTCCCCGT 138
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 163 TGCCTCTCTGGAGCAAGTGGTTCACTACTCTGGCCTTCCACGGTGGTGGTCTCTCA 222
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 139 ATGAGATGCTCGGGGCAAGGCTCGGTGTCCCA 172
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 223 CITAGATGCTGCTGGGAGCCCTTAGAGTCCCA 256
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
US-09-925-065A-916170
; Sequence 916170, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
```

```

; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 916170
; LENGTH: 629
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-916170

Query Match          10.3%; Score 30; DB 6; Length 629;
Best Local Similarity 53.4%; Pred. No. 13;
Matches 63; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 8 TTTATGTGCGTAGAACTAGTAGTGTGTTGCTGTGCGAATGACACTATGCAATGT 67
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 29 TTTATTTTCATAAAATGATGATTGCTATTGACATTTTCACATAGCAATTATGTTAAT 88
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 68 GATCTGGAACCTGGTTCTTGGGTGGGACGCTAGTTATGACTGTCGTCAGTAAATTT 125
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 89 CATATGGAATTTGAAATCTGGGAGTTTAACTTCTTTTCTGTTTTTCATTATATTT 146
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
US-09-925-065A-915272/c
; Sequence 915272, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 915272
; LENGTH: 634
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-915272

Query Match          10.3%; Score 30; DB 6; Length 634;
Best Local Similarity 53.4%; Pred. No. 13;
Matches 63; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 8 TTTATGTGCGTAGAACTAGTAGTGTGTTGCTGTGCGAATGACACTATGCAATGT 67
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 620 TTTATTTTCATAAAATGATGATTGCTATTGACATTTTCACATAGCAATTATGTTAAT 561
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 68 GATCTGGAACCTGGTTCTTGGGTGGGACGCTAGTTATGACTGTCGTCAGTAAATTT 125
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 560 CATATGGAATTTGAAATCTGGGAGTTTAACTTCTTTTCTGTTTTTCATTATATTT 503
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```


RESULT 12
US-11-124-368A-2913/c
; Sequence 2913, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2913
; LENGTH: 100000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-368A-2913

Query Match 10.3%; Score 30; DB 12; Length 100000;
Best Local Similarity 52.4%; Pred. No. 79;
Matches 66; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 152 GGGCAAGCCCTCGGTGCTCCACCTGTTGTGGCGGGGGCGCTGGAGCCCGGTCTGTT 211
Db 1981 GGGAGGGTCCCGGGGAGCTCGGGGGTGGGCTCGCGGGGCGCTGTTTGGGC 1922

Qy 212 GGGTTGGGAAGCCCTTTAACTGTGTGCTACCTGCTGCTTTTACCTTTTCATCGCTGTTAT 271
Db 1921 TGGAGCGTGGCCCGGGTGTGCTGTTACTGGGAGGTAGGCTTCTGCTGGGATTG 1862

Qy 272 TGTGAG 277
Db 1861 TGTGAG 1856

RESULT 13
US-09-925-065A-788291/c
; Sequence 788291, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 788291
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-788291

Query Match 10.2%; Score 29.8; DB 6; Length 630;

Best Local Similarity 55.2%; Pred. No. 15;
Matches 58; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 3 CCGGCTTTATGTCGTAGAAAAGTACTAGTGTGCTGTCGTAATGACACTATGC 62
Db 508 CAGGGATTATGTCGAGCGTAACCATCATCAACACTTGCATCGGAGATTCTTATCTTCA 449

Qy 63 AATGTGATCTGGAACCTGTTTCTTGGGTGGAGCCTAGTTATGA 107
Db 448 ACTCTGATCTTAAACTGCTTTCTGGAGTGTCTAGATAAGGATAA 404

RESULT 14
US-09-925-065A-709944/c
; Sequence 709944, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 709944
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-709944

Query Match 10.2%; Score 29.8; DB 6; Length 1149;
Best Local Similarity 52.0%; Pred. No. 19;
Matches 64; Conservative 1; Mismatches 58; Indels 0; Gaps 0;

Qy 152 GGGCAAGCCCTCGGTGCTCCACCTGTTGTGGCGGGGGCGCTGGAGCCCGGTCTGTT 211
Db 669 GTGTGAGACCTTGTCTCCCAACCCCTGATTGAGAACTCTGAGGATGGGATGKGTG 610

Qy 212 GGGTTGGGAAGCCCTTTAACTGTGTGCTACCTTTTACCTTTTTCATCGCTGTTAT 271
Db 609 GGGTTGGGTTCTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 550

Qy 272 TGT 274
Db 549 TTT 547

RESULT 15
US-10-750-185-50507/c
; Sequence 50507, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185

Wed Mar 8 09:43:21 2006

```
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50507
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Bovine 19866880889331
US-10-750-185-50507

Query Match      10.2%; Score 29.8; DB 8; Length 1785;
Best Local Similarity 60.5%; Pred. No. 22;
Matches 49; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 102 TTATGACTGTGCTCAGTAAATTTGGGGCTCCCGGTATGAGATGCTGCCGGGCAAGGCC 161
Db    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
740 TTAGGTTTGTAGTCAATTAAATTTCTGGACTACCCACATGCTATGCTGGGGAGCTTGGTC 681
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 162 TCGGTGTCCTCCACCTCGTTGT 182
Db    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 680 TCTGCCATTCAATATGTTAT 660
Db    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Search completed: March 8, 2006, 06:10:11
Job time : 776.844 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 04:11:07 ; Search time 629.177 Seconds
(without alignments)
3824.664 Million cell updates/sec

Title: US-10-603-524A-2

Perfect score: 291

Sequence: 1 agccggctttatgtcgtag.....tgtgagtggtcttatataca 291

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA_Main:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	291	100.0	291	7	US-10-603-524A-2
2	285.8	98.2	653	7	US-10-425-114-19731
3	285.8	98.2	1283	7	US-10-425-114-21156
4	260.2	89.4	733	7	US-10-425-114-32231
5	258.2	88.7	689	7	US-10-425-114-20758
6	253.2	87.0	752	7	US-10-425-114-32479
7	245.8	84.5	487	7	US-10-425-114-17184
8	221.4	76.1	267	7	US-10-424-599-14742
9	218.6	75.1	394	8	US-10-425-115-6597
10	217	74.6	1270	7	US-10-767-701-15432
11	206.2	70.9	464	8	US-10-425-115-153129
12	195.2	67.1	807	7	US-10-425-114-15469
13	195.2	67.1	824	7	US-10-425-114-25681
14	195.2	67.1	969	7	US-10-425-114-26566
15	195.2	67.1	1114	8	US-10-425-115-6593
16	189.6	65.2	283	8	US-10-425-115-76283
17	177.2	60.9	383	8	US-10-425-115-119075
18	172.2	59.2	378	8	US-10-425-115-14719
19	172.2	59.2	394	8	US-10-425-115-123144
20	170.2	58.5	385	8	US-10-425-115-162596
21	163.8	56.3	219	8	US-10-425-115-70427
22	160.2	55.1	303	8	US-10-425-115-147735
23	159.6	54.8	361	8	US-10-425-115-119871

ALIGNMENTS

RESULT 1

US-10-603-524A-2

; Sequence 2, Application US/10603524A

; Publication No. US20040158887A1

; GENERAL INFORMATION:

; APPLICANT: Dow AgroSciences LLC

; TITLE OF INVENTION: USE OF REGULATORY SEQUENCES IN TRANSGENIC PLANTS

; FILE REFERENCE: 50528A

; CURRENT APPLICATION NUMBER: US/10/603,524A

; CURRENT FILING DATE: 2003-06-25

; PRIOR APPLICATION NUMBER: 60/392571

; PRIOR FILING DATE: 2002-06-27

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 291

; TYPE: DNA

; ORGANISM: Zea mays

US-10-603-524A-2

Query Match

Beat Local Similarity 100.0%; Score 291; DB 7; Length 291;

Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AGCGGGCTTTATGTCGCTAGAACTAGTAGTAGTGTGCTGCTGGAATGACACTAT	60
Db	1	AGCGGGCTTTATGTCGCTAGAACTAGTAGTAGTGTGCTGCTGGAATGACACTAT	60
Qy	61	GCAATGTCATCTGGAACCTGGTTCTTCGGTGCAGCGTAGTATGACTGTCGTCAGTAA	120
Db	61	GCAATGTCATCTGGAACCTGGTTCTTCGGTGCAGCGTAGTATGACTGTCGTCAGTAA	120
Qy	121	AATTGGGGGCTCCCGGTATGAGATGCTGCGGGCAAGCCCTCGGTGTCACCTCGTTT	180
Db	121	AATTGGGGGCTCCCGGTATGAGATGCTGCGGGCAAGCCCTCGGTGTCACCTCGTTT	180
Qy	181	GTGGCGGGGGCGCTGGAGCCCGGTCTGGTGGGTGGGAAGCCCTTTAAACTGTGTCA	240
Db	181	GTGGCGGGGGCGCTGGAGCCCGGTCTGGTGGGTGGGAAGCCCTTTAAACTGTGTCA	240
Qy	241	CTTGCAATTTACCTTTTCATCGCTGTTTATGAGTGGTGCCTATATCAAA	291
Db	241	CTTGCAATTTACCTTTTCATCGCTGTTTATGAGTGGTGCCTATATCAAA	291

RESULT 2

US-10-425-114-19731
; Sequence 19731, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 19731
; LENGTH: 653
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3150-117-G4_FLI
US-10-425-114-19731

Query Match 98.2%; Score 285.8; DB 7; Length 653;
Best Local Similarity 99.3%; Pred. No. 2.8e-85;
Matches 287; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGCTGTGCTGCGAATGACACTAT 60
DB 365 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGCTGTGCTGCGAATGACACTAT 424
QY 61 GCAATGTGATCTGGAACCTGTTCTTGGTGGCGACGCTAGTATGACTGTGTCAGTAA 120
DB 425 GCAATGTGATCTGGAACCTGTTCTTGGTGGCGACGCTTGTATGACTGTGTCAGTAA 484
QY 121 AATTGGGGGCTCCCGGTATGAGATGCTGCGGGCAAGCCCTCGGTGTCACCTCGTTT 180
DB 485 AATTGGGGGCTCCCGGTATGAGATGCTGCGGGCAAGCCCTCGGTGTCACCTCGTTT 544
QY 181 GTGGCGGGGGCGCTGGAGCCCGCTGCTGTTGGTGGGAAGCCCTTTAAACTGTGTCA 240
DB 545 GTGGCGGGGGCGCTGGAGCCCGCTGCTGTTGGTGGGAAGCCCTTTAAACTGTGTCA 604
QY 241 CTTCGATTTTACCTTTTCCATCGCTGTTTATGAGTGGTCTTATATC 289
DB 605 CTTCGATTTTACCTTTTCCATCGCTGTTTATGAGTGGTCTTATATC 653

RESULT 3
US-10-425-114-21156
; Sequence 21156, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 21156
; LENGTH: 1283
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3279-175-F1_FLI
US-10-425-114-21156

Query Match 98.2%; Score 285.8; DB 7; Length 1283;
Best Local Similarity 99.3%; Pred. No. 3.6e-85;
Matches 287; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGCTGTGCTGCGAATGACACTAT 60
DB 995 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGCTGTGCTGCGAATGACACTAT 1054
QY 61 GCAATGTGATCTGGAACCTGTTCTTGGTGGCGACGCTAGTATGACTGTGTCAGTAA 120
DB 1055 GCAATGTGATCTGGAACCTGTTCTTGGTGGCGACGCTTGTATGACTGTGTCAGTAA 1114
QY 121 AATTGGGGGCTCCCGGTATGAGATGCTGCGGGCAAGCCCTCGGTGTCACCTCGTTT 180
DB 1115 AATTGGGGGCTCCCGGTATGAGATGCTGCGGGCAAGCCCTCGGTGTCACCTCGTTT 1174
QY 181 GTGGCGGGGGCGCTGGAGCCCGCTGCTGTTGGTGGGAAGCCCTTTAAACTGTGTCA 240
DB 1175 GTGGCGGGGGCGCTGGAGCCCGCTGCTGTTGGTGGGAAGCCCTTTAAACTGTGTCA 1234
QY 241 CTTCGATTTTACCTTTTCCATCGCTGTTTATGAGTGGTCTTATATC 289
DB 1235 CTTCGATTTTACCTTTTCCATCGCTGTTTATGAGTGGTCTTATATC 1283

RESULT 4
US-10-425-114-32231
; Sequence 32231, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 32231
; LENGTH: 733
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73277A08_FLI
US-10-425-114-32231
Query Match 89.4%; Score 260.2; DB 7; Length 733;
Best Local Similarity 94.6%; Pred. No. 1.2e-76;
Matches 283; Conservative 0; Mismatches 8; Indels 8; Gaps 1;
QY 1 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGCTGTGCTGCGAATGACACTAT 60
DB 396 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGCTGTGCTGCGAATGACACTAT 455
QY 61 GCAATGTGATCTGGAACCTGTTCTTGGTGGCGACGCT-----AGTTATGACTGTC 112
DB 456 GCAATGTGATCTGGAACCTGTTCTTGGTGGCGACGCTTTAGCCGTTGTTAGTCTGTC 515
QY 113 GTCAGTAAATTTGGGGGCTCCCGGTATGAGATGCTGCGGGCAAGCCCTCGGTGTCCA 172
DB 516 GTCCGTAATAATTTGGGGGCTCCCGGTAGGAGATGCTGCTGCGCAAGGCTCGGTGTCCA 575
QY 173 CCTCGTTTGTGGCGGGGCGCTGGAGCCCGCTGTTGGTGGGAGGAGCCCTTTAAAC 232
DB 576 CCTCGTGTGGCGGGGCGCTGGAGCCCGCTGTTGGTGGGAGGAGCCCTTTAAAC 635
QY 233 TGTGTGCACTTGTGCACTTTTACCTTTTCCATCGCTGTTTATGAGTGGTCTTATATCA 291

```
Db 636 TGTGTGCACTGCAATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTATATCAA 694
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73376G05_FLI
US-10-425-114-32479

Query Match 87.0%; Score 253.2; DB 7; Length 752;
Best Local Similarity 94.5%; Pred. No. 2.7e-74; Indels 8; Gaps 1;
Matches 276; Conservative 0; Mismatches 8; Indels 8; Gaps 1;

QY 1 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGTTTGTCTGCTGTCGAATGACACTAT 60
Db 461 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGTTTGTCTGCTGTCGAATGACACTAT 520
QY 61 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGACGCT-----AGTTATGACTGTC 112
Db 521 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGACGCTTGTAGCCGTGTTATGACTGTC 580
QY 113 GTCAGTAAATTTGGGGGCTCCCGTATGAGATGCTGCGGCAAGGCTCGGTGTCCTCA 172
Db 581 GTCAGTAAATTTGGGGGCTCCCGTATGAGATGCTGCGGCAAGGCTCGGTGTCCTCA 640
QY 173 CCTCGTTTGTGGCGGGGCGCTGAGGCGCGCTCTGGTTGGGTTGGGAAGCCCTTTAAAC 232
Db 641 CCTCGTTTGTGGCGGGGCGCTGAGGCGCGCTCTGGTTGGGTTGGGAAGCCCTTTAAAC 700
QY 233 TGTGTGCACTGCAATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTAT 284
Db 701 TGTGTGCACTGCAATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCT 752

RESULT 7
US-10-425-114-17184
; Sequence 17184, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 17184
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3068-038-B11_FLI
US-10-425-114-17184

Query Match 84.5%; Score 245.8; DB 7; Length 487;
Best Local Similarity 99.2%; Pred. No. 7e-72; Indels 2; Gaps 0;
Matches 247; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 1 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGTTTGTCTGCTGTCGAATGACACTAT 60
Db 239 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGTTTGTCTGCTGTCGAATGACACTAT 298
QY 61 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGACGCTAGTTATGACTGTCGTCAGTAA 120
Db 299 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGACGCTAGTTATGACTGTCGTCAGTAA 358
QY 121 AATTTGGGGGCTCCCGTATGAGATGCTGCGGGCAAGCCCTCGGTGTCCTCGTTT 180
Db 359 AATTTGGGGGCTCCCGTATGAGATGCTGCGGGCAAGCCCTCGGTGTCCTCGTTT 418
QY 181 GTGGCGGGGCGCTGAGGCGCGCTCTGTTGGGTTGGGAAGCCCTTTAAACCTGTTGCA 240
; LENGTH: 752
; TYPE: DNA
```

```
Db 636 TGTGTGCACTGCAATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTATATCAA 694
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73376G05_FLI
US-10-425-114-32479

Query Match 87.0%; Score 253.2; DB 7; Length 752;
Best Local Similarity 94.5%; Pred. No. 2.7e-74; Indels 8; Gaps 1;
Matches 276; Conservative 0; Mismatches 8; Indels 8; Gaps 1;

QY 1 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGTTTGTCTGCTGTCGAATGACACTAT 60
Db 461 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGTTTGTCTGCTGTCGAATGACACTAT 520
QY 61 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGACGCT-----AGTTATGACTGTC 112
Db 521 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGACGCTTGTAGCCGTGTTATGACTGTC 580
QY 113 GTCAGTAAATTTGGGGGCTCCCGTATGAGATGCTGCGGCAAGGCTCGGTGTCCTCA 172
Db 581 GTCAGTAAATTTGGGGGCTCCCGTATGAGATGCTGCGGCAAGGCTCGGTGTCCTCA 640
QY 173 CCTCGTTTGTGGCGGGGCGCTGAGGCGCGCTCTGGTTGGGTTGGGAAGCCCTTTAAAC 232
Db 641 CCTCGTTTGTGGCGGGGCGCTGAGGCGCGCTCTGGTTGGGTTGGGAAGCCCTTTAAAC 700
QY 233 TGTGTGCACTGCAATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTAT 284
Db 701 TGTGTGCACTGCAATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCT 752

RESULT 6
US-10-425-114-32479
; Sequence 32479, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 32479
; LENGTH: 752
; TYPE: DNA
```

Db 419 GTGGCGGGGGCGCTGGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAACTGTGTCA 478

Qy 241 CTTGCAATTT 249

Db 479 CTTGCAATTT 487

RESULT 8

US-10-424-599-14742
; Sequence 14742, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 14742
; LENGTH: 267
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_113318C.1
US-10-424-599-14742

Query Match 76.1%; Score 221.4; DB 7; Length 267;
Best Local Similarity 92.8%; Pred. No. 9e-64;
Matches 246; Conservative 0; Mismatches 11; Indels 8; Gaps 1;

Qy 14 TCGGTAGAACTAGTAGCTAGTGTGTTGCTGTGCAATGACACTATGCAATGTGATCTG 73

Db 1 TGCCTAGAACTAGTAGCTAGTGTGTTGCTGTGCAATGACACTATGCAATGTGATCTG 60

Qy 74 GAACCTGGTTCTCGGTGCGACGCT-----AGTTATGACTGCTCGTCAATAAATTT 125

Db 61 GAACCTGGTTCTCGGTGCGACGCTTGTAGCCGTGTATGACTGTGTCGCGTAAATTT 120

Qy 126 GGGGGCTCCCGCTATGAGATGCTGCGGCAAGGCTCGGTGTCACACTCGTTTGTGCGC 185

Db 121 GGGGGCTCCCGCTAAGGATGCTGCTGCAAGGCTCGGTGTCACACTCGTCTGTGCGC 180

Qy 186 GGGGGCGCTGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAACTGTTGTCACTTGC 245

Db 181 GTGGGGCGCTGGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAACTGTTGTCACTTGC 240

Qy 246 ATTTTACCTTTTCCATCGCTGTTTA 270

Db 241 ATTTTACCTTTTCCATCGCTGTTAA 265

RESULT 9

US-10-425-115-6597
; Sequence 6597, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 6597
; LENGTH: 394
; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_106008C.1

US-10-425-115-6597

Query Match 75.1%; Score 218.6; DB 8; Length 394;

Best Local Similarity 90.3%; Pred. No. 9e-63;

Matches 270; Conservative 0; Mismatches 19; Indels 10; Gaps 3;

Qy 1 AGCCGGCTTTATGTGCGTAGAACTAGTAGCTAGTGTGCTGTCGAATGACACTAT 60

Db 26 AGCCGGCTTTATGTGCGTAGAACTAGTAGCTAGTGTGCTGTCGAATGACACTAT 85

Qy 61 GCAATGTGATCTGGAACCTGGTTCTTGGGTGCGACGCT-----AGTTATGACTGTC 112

Db 86 GCAATGTGATCTGGAACCTGGTTCTTGGGTGCGACGCTTGTAGCCGTGTATGATATT 145

Qy 113 GTCAAGTAAATTTGGGGCTCCCGCTATGAGATGCTGCGGCAAGGCTCGGTGTCCCA 172

Db 146 GTCGGAAATTTGGGGCTCCCGCTATGAGATGCTGCGGCAAGGCTCGGTGTCCCA 205

Qy 173 CCTGTTGTGGCGGGGCGCTGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAAC 232

Db 206 CCTGTTGTGAGC-GGGGGCACTGGAGCCGCTGGTTGGGTGGGAAGCCCTTTAAAC 264

Qy 233 TGTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGTCTATATCAA 291

Db 265 TGTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGTCTATATCAA 322

RESULT 10

US-10-767-701-15432
; Sequence 15432, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 15432
; LENGTH: 1270
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CJUS49_330
US-10-767-701-15432

Query Match 74.6%; Score 217; DB 7; Length 1270;

Best Local Similarity 90.0%; Pred. No. 4.8e-62;

Matches 269; Conservative 0; Mismatches 20; Indels 10; Gaps 3;

Qy 1 AGCCGGCTTTATGTGCGTAGAACTAGTAGCTAGTGTGCTGTCGAATGACACTAT 60

Db 890 AGCCGGCTTTATGTGCGTAGAACTAGTAGCTAGTGTGCTGTCGAATGACACTAT 949

Qy 61 GCAATGTGATCTGGAACCTGGTTCTTGGGTGCGACGCT-----AGTTATGACTGTC 112

Db 950 GCAATGTGATCTGGAACCTGGTTCTTGGGTGCGACGCTTGTAGCCGTGTATGATATT 1009

Qy 113 GTCAAGTAAATTTGGGGCTCCCGCTATGAGATGCTGCGGCAAGGCTCGGTGTCCCA 172

Db 1010 GTCGGAAATTTGGGGCTCCCGCTATGAGATGCTGCGGCAAGGCTCGGTGTCCCA 1069

Qy 173 CCTGTTGTGGCGGGGCGCTGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAAC 232

Db 1070 CCTGTTGTGAGC-GGGGGCACTGGAGCCGCTGGTTGGGTGGGAAGCCCTTTAAAC 1128

Qy 233 TGTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGTCTATATCAA 291

```
Db 1129 TGTGTGACCTTGCACTTTTACCTTTT-CATCGCTGTTTATGTGAGTGGCTCTAAATCAA 1186
|||||
RESULT 11
US-10-425-115-153129
; Sequence 153129, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 153129
; LENGTH: 464
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MPT4577_71235C.1
US-10-425-115-153129
Query Match 70.9%; Score 206.2; DB 8; Length 464;
Best Local Similarity 86.3%; Pred. No. 1.4e-58;
Matches 251; Conservative 0; Mismatches 38; Indels 2; Gaps 2;
QY 1 AGCCGGCTTTATGTGCG-GTAGAACTAGTAGTGTGTTGCTGTGCTGTCGAATGACACTA 59
Db 173 AGCCGGCTTTATGTGCTGTACAACTAGTAGTGTGCTGTGCTGTGCTGTCGAATGACACTA 232
QY 60 TCGAATGTGATCTGGAACCTGTTCTTGGGTGCGAGCGTAGTGTATGACTGTGTCAGTA 119
Db 233 TCGAATGTGATCTGGAACCTGTTCTTGGGTGCGAGCGTAGTGTATGACTGTGTCAGTA 292
QY 120 AAATTGGGG-GCTCCCCCTATGAGATGCTGCGGGCGAAGGCTGCTGCTGCCACTCGT 178
Db 293 AAATTGGGGTGTCCCCACATGAGATGCTTCGGTACAGGCTGCTGACCACTGCTGC 352
QY 179 TTGTGCGGGGGCGCTGAGCGCCGCTGTGTTGGGTGGGAAGCCCTTTAAACTGTTGT 238
Db 353 TTGAGACGGGGGGCGCTGCAACCCGACTGGTAGATATCGGAAGCCCTTTAAACTGTTGT 412
QY 239 CACTTGCATTTTACCTTTTCCATCGCTGTTTATTTGAGTGTGCTATATC 289
Db 413 TACTTGCATTTTACCTTTTCCATCGCTGTTTATTTGCGAGGGGCCCTATATC 463
RESULT 12
US-10-425-114-15469
; Sequence 15469, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 15469
; LENGTH: 807
; TYPE: DNA
; ORGANISM: Zea mays
```

```
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3060-005-C4_FLI
US-10-425-114-15469
Query Match 67.1%; Score 195.2; DB 7; Length 807;
Best Local Similarity 81.5%; Pred. No. 8.6e-55;
Matches 243; Conservative 0; Mismatches 43; Indels 12; Gaps 1;
QY 1 AGCCGGCTTTATGTGCGTAGAACTAGTAGTGTGTTGCTGCTGCTGCAATGACACTAT 60
Db 489 AGCCGGCTTTATGTGCGTAGAACTAGTAGTGTGTTGCTGCTGCTGCAATGACACTAT 548
QY 61 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGAGCGCTGTAGCAGCGCTGTATGATT 110
Db 549 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGAGCGCTGTAGCAGCGCTGTATGATT 608
QY 111 --TCGTGAGTAAATTTGGGGGCTCCCGTATGAGATGCTGCGGCAAGGCTCGGTCT 168
Db 609 ATTTGTGGGAAATTTGGGGGCTCCCATATGAGATGCTGCGGCAAGACTCGGCAT 668
QY 169 CCCACCTCGTTTGTGCGGGGGCGCTGGAGCCCGCTCTGTTGGGTGGGAAGCCCTTT 228
Db 669 CCCACCTCGTTTGTGCGGGGGCGCTGGAGCGCTGTTGGGTGGGAAGCCCTTT 728
QY 229 AAATCTGTTGTCATCTTGCATTTTACCTTTTCCATCGCTGTTTATTTGAGTGTGCTAT 286
Db 729 AAATCTGTTGTCGCTTGCATTTTAACTTTTCACTGCGCTTCACTGCTCTATAATCTAT 786
RESULT 13
US-10-425-114-25681
; Sequence 25681, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 25681
; LENGTH: 824
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3957-025-B7_FLI
US-10-425-114-25681
Query Match 67.1%; Score 195.2; DB 7; Length 824;
Best Local Similarity 81.5%; Pred. No. 8.6e-55;
Matches 243; Conservative 0; Mismatches 43; Indels 12; Gaps 1;
QY 1 AGCCGGCTTTATGTGCGTAGAACTAGTAGTGTGTTGCTGCTGCTGCAATGACACTAT 60
Db 504 AGCCGGCTTTATGTGCGTAGAACTAGTAGTGTGTTGCTGCTGCTGCAATGACACTAT 563
QY 61 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGAGCGCTGTAGCAGCGCTGTATGATT 110
Db 564 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGAGCGCTGTAGCAGCGCTGTATGATT 623
QY 111 --TCGTGAGTAAATTTGGGGGCTCCCGTATGAGATGCTGCGGCAAGGCTCGGTCT 168
Db 624 ATTTGTGGGAAATTTGGGGGCTCCCATATGAGATGCTGCGGCAAGACTCGGCAT 683
QY 169 CCCACCTCGTTTGTGCGGGGGCGCTCGAGCCCGCTGAGTGTGTTGGGTGGGAAGCCCTTT 228
Db 684 CCCACCTCGTTTGTGCGGGGGCGCTCGAGCGCTGAGTGTGTTGGGTGGGAAGCCCTTT 743
```


GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 03:46:27 ; Search time 336.308 Seconds
(without alignments)
5766.810 Million cell updates/sec

Title: US-10-603-524A-2
Perfect score: 291
Sequence: 1 acccgctttatgtcgtag.....tgtgagtggtctatatcaaa 291

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4995997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	291	100.0	291	12 ADI22023	ADI22023 Maize 3'
2	285.8	98.2	653	13 ADX36911	Adx36911 Plant ful
3	285.8	98.2	1283	13 ADX46416	Adx46416 Plant ful
4	260.2	89.4	733	13 ADX61388	Adx61388 Plant ful
5	258.2	88.7	689	13 ADX46018	Adx46018 Plant ful
6	253.2	87.0	752	13 ADX61836	Adx61836 Plant ful
7	245.8	84.5	487	13 ADX34364	Adx34364 Plant ful
8	195.2	67.1	807	13 ADX32649	Adx32649 Plant ful
9	195.2	67.1	824	13 ADX50941	Adx50941 Plant ful
10	195.2	67.1	969	13 ADX51916	Adx51916 Plant ful
11	33.8	11.6	76201	12 ADJ62814	Adj62814 Human ORF
12	33.6	11.5	378	6 ABN79028	Abn79028 Human ORF
13	33.2	11.4	56826	13 ABD33496	Abd33496 Human can
14	32.8	11.3	3879	4 ABL27441	Abi27441 Drosophil
15	32.8	11.3	6613	4 ABL27440	Abi27440 Drosophil
16	32.4	11.1	516	11 ABD17758	Abd17758 Pseudomon
17	32.4	11.1	846	11 ABD17867	Abd17867 Pseudomon
18	32.4	11.1	885	11 ABD17526	Abd17526 Pseudomon
19	32.2	11.1	582	5 ABV56992	Abv56992 Human pro

20	32.2	11.1	1253	11 ACN83015	ACn83015 Breast ca
21	32	11.0	225883	13 ADV34981	Adv34981 Murine CD
c 22	31.4	10.8	462	5 ABV51301	Abv51301 Human pro
c 23	31.2	10.7	3372	6 ABK31761	Abk31761 DNA encod
c 24	31.2	10.7	3492	6 ABQ75954	Abq75954 Human PPM
c 25	31.2	10.7	20097	12 ADP47968	Adp47968 Human MRC
c 26	31.2	10.7	65140	4 AAD17184	Aad17184 Streptomy
c 27	31.2	10.7	125401	4 AAD17186	Aad17186 Streptomy
c 28	31	10.7	1650	13 ADT19187	Adt19187 Plant CDN
c 29	31	10.7	1704	8 ACA25640	ACA25640 Prokaryot
c 30	31	10.7	1752	8 ACA25826	ACA25826 Prokaryot
c 31	31	10.7	47686	12 ADQ59461	Adq59461 Human can
c 32	31	10.7	47774	14 ADZ13790	Adz13790 Murine can
c 33	30.8	10.6	515	6 ABQ44818	Abq44818 Oligonucle
c 34	30.8	10.6	515	6 ABQ44819	Abq44819 Oligonucle
c 35	30.8	10.6	516	6 ABQ21873	Abq21873 Oligonucle
c 36	30.8	10.6	516	6 ABQ21872	Abq21872 Oligonucle
c 37	30.8	10.6	531	6 ABQ16314	Abq16314 Oligonucle
c 38	30.8	10.6	531	6 ABQ16315	Abq16315 Oligonucle
c 39	30.8	10.6	532	6 ABQ50428	Abq50428 Oligonucle
c 40	30.8	10.6	532	6 ABQ50429	Abq50429 Oligonucle
c 41	30.8	10.6	858	14 ADZ64183	Adz64183 Human can
c 42	30.8	10.6	1321	11 ACL32346	ACL32346 Rice abio
c 43	30.8	10.6	2973	13 ADT20151	Adt20151 Plant CDN
c 44	30.8	10.6	3898	12 ADQ63136	Adq63136 Novel hum
c 45	30.8	10.6	7752	2 AAV38365	AAv38365 Mouse ESX

ALIGNMENTS

RESULT 1
ADI22023
ID ADI22023 standard; DNA; 291 BP.

AC ADI22023;

DT 22-APR-2004 (first entry)

DE Maize 3' UTR #2.

XX ss; 3' untranslated region; UTR; expression cassette; transformed plant;
KW promoter; untranslated leader sequence; genetic engineering.

XX Zea mays.

OS WO2004003177-A2.

PN 08-JAN-2004.

XX 25-JUN-2003; 2003WO-US020977.

XX 27-JUN-2002; 2002US-0392571P.

XX (DOWC) DOW AGROSCIENCES LLC.

XX Cowen NW, Smith KA, Armstrong K;

XX WPI; 2004-071986/07.

XX New isolated DNA molecule useful for genetic engineering of plants or for
PT improving the expression of transgenes in plants, particularly corn
plants.

XX Claim 1; SEQ ID NO 2; 20pp; English.

XX This sequence represents a 3' untranslated region (UTR) which was used in
CC the construction of the recombinant expression cassette of the invention.
CC The expression cassette is for effecting expression of a foreign gene in
CC a transformed plant and comprises a promoter operable in plants, an
CC untranslated leader sequence, a foreign gene of interest, and a 3'UTR.
CC This cassette may be used to transform plants, for genetic engineering of
CC plants or in improving the expression of transgenes in plants.


```
XX 28-APR-2003; 2003US-00425114.
XX AC
XX 06-MAY-1999; 99US-00304517.
XX DT
XX 05-NOV-2001; 2001US-00985678.
XX DE
XX (LIU/J) LIU J.
XX PA
XX (ZHOU/J) ZHOU Y.
XX PA
XX (KOVA/J) KOVALIC D K.
XX PA
XX (SCRE/J) SCREEN S E.
XX PA
XX (TABA/J) TABASKA J E.
XX PA
XX (CAOY/J) CAO Y.
XX PI
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX pests, for conferring increased resistance to plant disease, or for
XX improving yield.
XX
XX Claim 1; SEQ ID NO 21156; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
XX of the invention are also useful in physical arrays of molecules and as
XX plant breeding markers. The recombinant DNA construct is useful for
XX improving plant tolerance to cold, heat, drought, herbicides, extreme
XX osmotic conditions, pathogens or pests, for manipulating growth rate in
XX plant cells by modification of the cell cycle pathway, for conferring
XX increased resistance to plant disease, for producing galactomannan,
XX lignin or plant growth regulators, for increasing the rate of homologous
XX recombination in plants, for improving yield by modification of
XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX or by providing improved plant growth and development under at least one
XX stress condition or for modifying seed oil or protein yield and/or
XX content. This sequence represents a plant full length insert
XX polynucleotide that can be used in the recombinant DNA construct of the
XX invention.
XX
XX Sequence 1283 BP; 287 A; 333 C; 369 G; 294 T; 0 U; 0 Other;
XX
XX Query Match 98.2%; Score 285.8; DB 13; Length 1283;
XX Best Local Similarity 99.3%; Pred. No. 7.5e-84;
XX Matches 287; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 AGCCGGCTTTATGTCGTTAGAACTAGTAGTAGTGTGTTGCTGTCGTAATGACACTAT 60
XX 995 AGCCGGCTTTATGTCGTTAGAACTAGTAGTAGTGTGTTGCTGTCGTAATGACACTAT 1054
XX
XX 61 GCAATGTGATCTGGACCTGTTTCTTGGTGGCGAGCGCTAGTATGACTGTCGTAAT 120
XX 1055 GCAATGTGATCTGGACCTGTTTCTTGGTGGCGAGCGCTAGTATGACTGTCGTAAT 1114
XX
XX 121 AATTGGGGGGCTCCCGTATGAGATGCTGCGGGCAAGCGCTCGGTGTCACCTCGTTT 180
XX 1115 AATTGGGGGGCTCCCGTATGAGATGCTGCGGGCAAGCGCTCGGTGTCACCTCGTTT 1174
XX
XX 181 GTGGCGGGGGCGCTGGAGCCCGGCTGTTGGTGGGTGGGAAGCCCTTTAAACTGTTGCA 240
XX 1175 GTGGCGGGGGCGCTGGAGCCCGGCTGTTGGTGGGTGGGAAGCCCTTTAAACTGTTGCA 1234
XX
XX 241 CTGCAATTTTACCTTTTCCATCGCTGTTTATGTAGTGGTCTATATC 289
XX
XX 1235 CTGCAATTTTACCTTTTCCATCGCTGTTTATGTAGTGGTCTATATC 1283
```

RESULT 4

ADXG1388

ID ADXG1388 standard; cDNA; 733 BP.

```
XX ADXG1388;
XX 21-APR-2005 (first entry)
XX DE
XX Plant full length insert polynucleotide seqid 32231.
XX
XX plant protectant; plant growth regulant; gene therapy; plant;
XX recombinant DNA construct; physical array; plant breeding marker;
XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX extreme osmotic condition; pathogen tolerance; pest tolerance;
XX growth rate; cell cycle pathway; disease resistance;
XX galactomannan production; lignin production; plant growth regulator;
XX yield; plant growth; plant development; seed oil; protein yield;
XX protein content; gene; ss.
XX
XX Unidentified.
XX
XX US2004034888-A1.
XX
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
XX 05-NOV-2001; 2001US-00985678.
XX
XX (LIU/J) LIU J.
XX (ZHOU/J) ZHOU Y.
XX (KOVA/J) KOVALIC D K.
XX (SCRE/J) SCREEN S E.
XX (TABA/J) TABASKA J E.
XX (CAOY/J) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX pests, for conferring increased resistance to plant disease, or for
XX improving yield.
XX
XX Claim 1; SEQ ID NO 32231; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
XX of the invention are also useful in physical arrays of molecules and as
XX plant breeding markers. The recombinant DNA construct is useful for
XX improving plant tolerance to cold, heat, drought, herbicides, extreme
XX osmotic conditions, pathogens or pests, for manipulating growth rate in
XX plant cells by modification of the cell cycle pathway, for conferring
XX increased resistance to plant disease, for producing galactomannan,
XX lignin or plant growth regulators, for increasing the rate of homologous
XX recombination in plants, for improving yield by modification of
XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX or by providing improved plant growth and development under at least one
XX stress condition or for modifying seed oil or protein yield and/or
XX content. This sequence represents a plant full length insert
XX polynucleotide that can be used in the recombinant DNA construct of the
XX invention.
XX
XX Sequence 733 BP; 150 A; 176 C; 208 G; 199 T; 0 U; 0 Other;
XX
XX Query Match 89.4%; Score 260.2; DB 13; Length 733;
XX Best Local Similarity 94.6%; Pred. No. 1.8e-75;
XX Matches 283; Conservative 0; Mismatches 8; Indels 8; Gaps 1;
XX
XX 1 AGCCGGCTTTATGTCGTTAGAACTAGTAGTAGTGTGTTGCTGTCGTAATGACACTAT 60
XX 396 AGCCGGCTTTATGTCGTTAGAACTAGTAGTAGTGTGTTGCTGTCGTAATGACACTAT 455
```


PA (TAB//) TABASKA J E.
 PA (CAOY//) CAO Y.
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JB, Cao Y;
 PI WPI; 2004-180133/17.
 XX
 XX New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 PS Claim 1; SEQ ID NO 32479; 15pp; English.
 XX
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.
 XX
 SQ Sequence 752 BP; 154 A; 190 C; 210 G; 198 T; 0 U; 0 Other;
 Query Match 87.0%; Score 253.2; DB 13; Length 752;
 Best Local Similarity 94.5%; Pred. No. 3.8e-73;
 Matches 276; Conservative 0; Mismatches 8; Indels 8; Gaps 1;
 QY 1 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGCTGTGCTGCGAATGACACTAT 60
 Db 461 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGCTGTGCTGCGAATGACACTAT 520
 QY 61 GCAATGTGATCTGGAACCTGCTTTCTTGGTCCGACGCTTGTAGCGGTGTATGACTGTC 112
 Db 521 GCAATGTGATCTGGAACCTGCTTTCTTGGTCCGACGCTTGTAGCGGTGTATGACTGTC 580
 QY 113 GTCATAAAATTTGGGGCTCCCGTATGAGATGCTGCGGCAAGGCTCGGTGCCA 172
 Db 581 GTCATAAAATTTGGGGCTCCCGTATGAGATGCTGCGGCAAGGCTCGGTGCCA 640
 QY 173 CCTCGTTTGTGGCGGGGCGCTGAGGCCCGGTCTGTTGGTGGGAGCCCTTTAAAC 232
 Db 641 CCTCGTTTGTGGCGGGGCGCTGAGGCCCGGTCTGTTGGTGGGAGCCCTTTAAAC 700
 QY 233 TGTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATGTGAGTGGTCT 284
 Db 701 TGTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATGTGAGTGGTCT 752
 RESULT 7
 ADX34364
 ID ADX34364 standard; cDNA; 487.BP.
 XX
 AC ADX34364;
 XX
 XX 21-APR-2005 (first entry)
 DT
 XX Plant full length insert polynucleotide seqid 17184.
 DE
 XX plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

extreme osmotic condition; pathogen tolerance; pest tolerance;
 growth rate; cell cycle pathway; disease resistance;
 galactomannan production; lignin production; plant growth regulator;
 yield; plant growth; plant development; seed oil; protein yield;
 protein content; gene; ss.
 Unidentified.
 US2004034888-A1.
 19-FEB-2004.
 28-APR-2003; 2003US-00425114.
 06-MAY-1999; 99US-00304517.
 05-NOV-2001; 2001US-00985678.
 (LIU//) LIU J.
 (ZHOU//) ZHOU Y.
 (KOVA//) KOVALIC D K.
 (SCRE//) SCREEN S E.
 (TAB//) TABASKA J E.
 (CAOY//) CAO Y.
 Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JB, Cao Y;
 WPI; 2004-180133/17.
 New recombinant DNA construct, useful for improving plant tolerance to
 cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 pests, for conferring increased resistance to plant disease, or for
 improving yield.
 Claim 1; SEQ ID NO 17184; 15pp; English.
 The invention describes a recombinant DNA construct comprising a
 polynucleotide consisting of a sequence encoding an amino acid sequence
 available in electronic form from the US patent office at
 ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 of the invention are also useful in physical arrays of molecules and as
 plant breeding markers. The recombinant DNA construct is useful for
 improving plant tolerance to cold, heat, drought, herbicides, extreme
 osmotic conditions, pathogens or pests, for manipulating growth rate in
 plant cells by modification of the cell cycle pathway, for conferring
 increased resistance to plant disease, for producing galactomannan,
 lignin or plant growth regulators, for increasing the rate of homologous
 recombination in plants, for improving yield by modification of
 photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 or by providing improved plant growth and development under at least one
 stress condition or for modifying seed oil or protein yield and/or
 content. This sequence represents a plant full length insert
 polynucleotide that can be used in the recombinant DNA construct of the
 invention.
 Sequence 487 BP; 99 A; 118 C; 143 G; 127 T; 0 U; 0 Other;
 Query Match 84.5%; Score 245.8; DB 13; Length 487;
 Best Local Similarity 99.2%; Pred. No. 8.8e-71;
 Matches 247; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGCTGTGCTGCGAATGACACTAT 60
 Db 239 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGCTGTGCTGCGAATGACACTAT 298
 QY 61 GCAATGTGATCTGGAACCTGCTTTCTTGGTGGCGACGCTTGTATGACTGTCGTAGTAA 120
 Db 299 GCAATGTGATCTGGAACCTGCTTTCTTGGTGGCGACGCTTGTATGACTGTCGTAGTAA 358
 QY 121 AATTTGGGGCTCCCGTATGAGATGCTGCGGCAAGGCTCGGTGCCACCTCGTTT 180
 Db 359 AATTTGGGGCTCCCGTATGAGATGCTGCGGCAAGGCTCGGTGCCACCTCGTTT 418
 QY 181 GTGGCGGGGGCGCTGGAGCCCGGTCTGTTGGGTGGGAAGCCCTTTAAACTGTTGTCA 240

PT improving yield.
 XX
 PS Claim 1; SEQ ID NO 25681; 15pp; English.
 XX

The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.segdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomanan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the invention.

XX
 SQ Sequence 824 BP; 178 A; 216 C; 218 G; 212 T; 0 U; 0 Other;
 XX

Query Match 67.1%; Score 195.2; DB 13; Length 824;
 Best Local Similarity 81.5%; Pred. No. 6.3e-54;
 Matches 243; Conservative 0; Mismatches 43; Indels 12; Gaps 1;

QY 1 AGCCGGCTTTATGTCGTAGAACTAGTAGTGTGTTGCTGCTGCAATGACACTAT 60
 DB 504 AGCCGGCTTTATGTCGTAGAACTAGTAGTGTGTTGCTGCTGCAATGACACTAT 563

QY 61 GCAATGTGATCTGGAACTGCTGTTCTTGGTGGCGGACGCTGATGATGACTG 110
 DB 564 GCAATGTGATCTGGAACTGCTGTTCTTGGTGGCGGACGCTGATGATGACTG 623

QY 111 --TCGTAGTAAATTTGGGGGCTCCCGTATGAGATGTCGCGGCAAGCGCTCGGTG 168
 DB 624 ATTTGTCGGGAAATTTGGGGGCTCCCGTATGAGATGTCGCGGCAAGCGCTCGGCAT 683

QY 169 CCCACTGTTGTCGGGGGGGCGCTGAGCCGCTGCTGTTGGTGGGAGCCCTTT 228
 DB 684 CCCACTGTTGTCGGGGGGGCGCTGAGCCGCTGCTGTTGGTGGGAGCCCTTT 743

QY 229 AAATGTTGTCACTTGCACTTTTACCTTTTCCATCGCTGTTTATGTGAGTGTCTAT 286
 DB 744 AAATGTTGTCTGCTTGCACTTTTAACTTTTCAATCGCGTTCAGTGTCTTAATCTAT 801

RESULT 10
 ADX51916
 ID ADX51916 standard; cDNA; 969 BP.
 XX
 AC ADX51916;
 XX
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Plant full length insert polynucleotide seqid 26656.
 XX
 KW plant protectant; plant growth regulator; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomanan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content; gene; ss.
 XX
 OS Unidentified.
 XX
 OS
 PN US2004034888-A1.
 XX

PD 19-FEB-2004.
 XX
 PF 28-APR-2003; 2003US-00425114.
 XX
 PR 06-MAY-1999; 99US-00304517.
 PR 05-NOV-2001; 2001US-00985678.
 XX
 PA (LIU//) LIU J.
 PA (ZHOU//) ZHOU Y.
 PA (KOVA//) KOVALIC D K.
 PA (SCRE//) SCREEN S E.
 PA (TABA//) TABASKA J E.
 PA (CAOY//) CAO Y.
 XX
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 WPI; 2004-180133/17.
 XX
 DR New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 PS Claim 1; SEQ ID NO 26656; 15pp; English.
 XX

The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.segdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomanan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the invention.

XX
 SQ Sequence 969 BP; 218 A; 238 C; 269 G; 244 T; 0 U; 0 Other;
 XX

Query Match 67.1%; Score 195.2; DB 13; Length 969;
 Best Local Similarity 81.5%; Pred. No. 6.7e-54;
 Matches 243; Conservative 0; Mismatches 43; Indels 12; Gaps 1;

QY 1 AGCCGGCTTTATGTCGTAGAACTAGTAGTGTGTTGCTGCTGCAATGACACTAT 60
 DB 634 AGCCGGCTTTATGTCGTAGAACTAGTAGTGTGTTGCTGCTGCAATGACACTAT 693

QY 61 GCAATGTGATCTGGAACTGCTGTTCTTGGTGGCGGACGCTGATGATGACTG 110
 DB 694 GCAATGTGATCTGGAACTGCTGTTCTTGGTGGCGGACGCTGATGATGACTG 753

QY 111 --TCGTAGTAAATTTGGGGGCTCCCGTATGAGATGTCGCGGCAAGCGCTCGGTG 168
 DB 754 ATTTGTCGGGAAATTTGGGGGCTCCCGTATGAGATGTCGCGGCAAGCGCTCGGCAT 813

QY 169 CCCACTGTTGTCGGGGGGGCGCTGAGCCGCTGCTGTTGGTGGGAGCCCTTT 228
 DB 814 CCCACTGTTGTCGGGGGGGCGCTGAGCCGCTGCTGTTGGTGGGAGCCCTTT 873

QY 229 AAATGTTGTCACTTGCACTTTTACCTTTTCCATCGCTGTTTATGTGAGTGTCTAT 286
 DB 874 AAATGTTGTGCTTGCACTTTTAACTTTTCAATCGCGCTTCAGTGTCTTAATCTAT 931

RESULT 11
 ADJ62814/c

ID ADJ62814 standard; cDNA; 76201 BP.
 AC ADJ62814;
 XX 06-MAY-2004 (first entry)
 DT Human cDNA differentially expressed in response to docetaxel #84.
 DE array; docetaxel; docetaxel resistance; cancer; human; ss;
 KW differential expression.
 KW Homo sapiens.
 XX OS
 XX US2004018527-A1.
 PN 29-JAN-2004.
 PD 16-MAY-2003; 2003US-00439703.
 XX 17-MAY-2002; 2002US-0381141P.
 XX (CHAN/) CHANG J C.
 PA (OCON/) O'CONNELL P.
 XX Chang JC, O'Connell P;
 PI WPI; 2004-224389/21.
 DR Array useful for screening patient for resistance to docetaxel comprises
 PT complementary nucleic acid probes attached to solid surface.
 XX Claim 21; SEQ ID NO 84; 169pp; English.
 PS The invention relates to an array for screening a patient for resistance
 XX to docetaxel comprising complementary nucleic acid probes attached to a
 CC solid surface for at least 10 of the nucleic acids chosen from 91 fully
 CC defined sequences as given in the specification. The array is useful for
 CC screening a patient for resistance to docetaxel. The array is also useful
 CC for monitoring a cancer patient receiving docetaxel therapy. The present
 CC sequence represents a human cDNA differentially expressed in response to
 CC docetaxel.
 XX Sequence 76201 BP; 19685 A; 17309 C; 18629 G; 20578 T; 0 U; 0 Other;
 SQ Query Match 11.6%; Score 33.8; DB 12; Length 76201;
 Best Local Similarity 64.9%; Pred. No. 12;
 Matches 50; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
 QY 147 CTGCGGGCAAGCGCTCGGTGTCACCTGTCGGGGGGGGCGTGGAGCCCGTTC 206
 Db 12996 CGGCGGGATTGCTCTGTCGTCCTCCCGGCGGGGAGTGGGGGGCGGGCGGCG 12937
 QY 207 TGGTTGGTTGGGAAGC 223
 Db 12936 TGGGAGGTTTGAAGAAGC 12920
 RESULT 12
 ABN79028/c
 ID ABN79028 standard; cDNA; 378 BP.
 XX AC
 XX ABN79028;
 XX 08-JUL-2002 (first entry)
 DT Human ORF3975 cDNA, SEQ ID NO:7949.
 DE Human; ORF; open reading frame; ORFX; drug screening; diagnosis;
 KW disease monitoring; cytokine; cell proliferation; cell differentiation;
 KW immune modulation; haematopoiesis regulation; tissue growth;
 KW angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;
 KW thrombolytic; tumour inhibition; bodily characteristic; fertility;
 KW behaviour; cancer; proliferative disorder; neurological disorder;

KW cardiovascular disease; immune system disorder; organ transplantation;
 KW tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
 KW hypothyroidism; cholesterol ester storage disease; infection; vulnery;
 KW vasotropic; antipsoriatic; antidiabetic; cycostatic; nootropic;
 KW neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;
 KW cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator;
 KW dermatological; analgesic; virucide; antibacterial; fungicide; gene; ss.
 XX Homo sapiens.
 XX WO200190366-A2.
 PN 29-NOV-2001.
 XX 24-MAY-2001; 2001WO-US017076.
 PF 24-MAY-2000; 2000US-0206690P.
 XX (CURA-) CURAGEN CORP.
 XX Leach MD, Shimkets RA;
 PI WPI; 2002-106200/14.
 DR P-PSDB; ABP35002.
 XX Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and disorders related to organ
 PT transplantation.
 XX Claim 1; Page 2233; 2508pp; English.
 PS Sequences ABP31028-ABP35561 represent 4534 novel human proteins
 CC designated ORF (open reading frame) 1-4534, and sequences ABN75054-
 CC ABN79587 represent cDNAs encoding them. The invention also encompasses
 CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
 CC referred to as ORFX) proteins, polynucleotides at least 85% identical to
 CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
 CC polynucleotides, the recombinant production of ORFX proteins, antibodies
 CC specific for ORFX proteins, methods of detecting ORFX polynucleotides and
 CC polypeptides, methods of screening for modulators of ORFX expression or
 CC activity, and methods of screening individuals for a predisposition to an
 CC ORFX-associated disorder. The ORFX proteins of the invention have a wide
 CC range of biological activities, such as cytokine, cell proliferation,
 CC cell differentiation, immune modulation, haematopoiesis regulation,
 CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
 CC chemokinetic activity, haemostatic activity, thrombolytic activity,
 CC receptor/ligand, antiinflammatory activity, tumour inhibition activity,
 CC and antiinfective activity, and may also be involved in the determination
 CC of bodily characteristics, fertility and behaviour. ORFX proteins,
 CC nucleic acids and antibodies may be used in the treatment of cancers,
 CC other proliferative disorders such as psoriasis and benign tumours,
 CC neurological disorders such as epilepsy and Alzheimer's disease,
 CC cardiovascular diseases, immune system disorders, disorders related to
 CC organ transplantation, disorders of tissue growth and regeneration,
 CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester
 CC storage disease, and infectious diseases caused by viral, bacterial,
 CC fungal and other pathogens. ORFX nucleic acids may also be used as a
 CC source of primers and probes, in the detection of ORFX genomic sequences
 CC or transcripts, in the identification and cloning of homologous
 CC sequences, in genetic diagnosis, and in forensic biology. The ORFX
 CC nucleic acids may additionally be used to produce transgenic animals
 CC which may be useful for studying the function and/or activity of ORFX
 CC protein, and in drug screening. The ORFX proteins may also be used as
 CC immunogens to generate specific antibodies, which are useful in the
 CC diagnosis, treatment and monitoring of ORFX-associated diseases
 XX SQ Sequence 378 BP; 61 A; 122 C; 150 G; 42 T; 0 U; 3 Other;
 Query Match 11.5%; Score 33.6; DB 6; Length 378;
 Best Local Similarity 53.5%; Pred. No. 1.5;
 Matches 69; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy	151	CGGGCAAGCCCTCGGTGTC	CCCACTCGCTTTCTGCGGGGGGCGCTGGAGCCCGCTCTGT	210
Db	321	CGGGCAATGCCCTTGGAGAGCT	CCCCCTTCTCTCGGGGTGTGCCCCAGAGGCCCAATCTGC	262
Qy	211	TGGGTGGGAAGCCCTTTAAACTGTGTGCA	CTTGCACTTGCACTTTTACCTTTTTCATCGCTGTTTA	270
Db	261	GGGGGTGGGAACCTGGAGCCCCCTTCTCCGGGGACGTGACCTGTGAGCTCCACTTTTC		202
Qy	271	TTGTGAGTG	279	
Db	201	CCGAGGGGG	193	

RESULT 13	
ABD33496/c	
ID ABD33496 standard; DNA; 56826 BP.	
XX	
XX	
AC ABD33496;	
XX	
DT 18-NOV-2004 (first entry)	
XX	
XX	Human cancer-associated (CA) gene HD07-096.
DE	
XX	
XX	Human; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
KW	
KW	de; cancer; cytostatic.
XX	
XX	Homo sapiens.
OS	
XX	
XX	WO2004058146-A2.
PN	
PD	
PD	15-JUL-2004.
XX	
XX	15-DEC-2003; 2003WO-US040081.
PF	
XX	
XX	17-DEC-2002; 2002US-00322281.
PR	
XX	(SAGR-) SAGRES DISCOVERY INC.
PA	
XX	
XX	Morris DW, Malandro MS;
PI	
XX	WPI; 2004-499109/47.
XX	
DR	

Qy 181 GTGGCGGGGCGCTGAGCCGGTCGTGTTGGG 214
||| ||| ||| ||| ||| ||| ||| ||| |||
Dδ 10198 GGGGTCGGGGGCTCTGGGCTCTGCCTAGCGTGG 10165
||||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 14
ABL27441/c
ID ABL27441 standard; DNA; 3879 BP.
XX AC
XX ABL27441;
XX 26-MAR-2002 (first entry)
XX DT
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 33796.
XX DE
XX Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical; gene; ds.
XX KW
XX Drosophila melanogaster.
XX OS
XX WO200171042-A2.
XX PN
XX 27-SEP-2001.
XX PD
XX 23-MAR-2001; 2001WO-US009231.
XX PF
XX 23-MAR-2000; 2000US-0191637P.
XX PR
XX 11-JUL-2000; 2000US-00614150.
XX PR
XX (PEKE ) PE CORP NY.
XX PA
XX Venter JC, Adams M, Li PWD, Myers EW;
XX PI
XX WPI; 2001-656860/75.
XX DR
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signaling and cell-cell
XX PT interactions.
XX PT
XX
XX Claim 1; SEQ ID NO 33796; 2ipp + Sequence Listing; English.
XX PS
XX The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX CC sequences (ABL01840-ABL16175) and the encoded proteins (AB57737-
XX CC AB572072). The sequence data for this patent did not form part of the
XX CC printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ
XX Sequence 3879 BP; 1070 A; 1069 C; 979 G; 761 T; 0 U; 0 Other;
XX
XX Query Match 11.3%; Score 32.8; DB 4; Length 3879;
XX Best Local Similarity 53.0%; Pred. NO. 7.2;
XX Matches 70; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
XX
XX QY 55 CACTATGCAATGTGATCTGGAACCTCGTTTCTTTGGGTGGGACGCTAGTTATGACTGTGCT 114
XX DB 1285 CACTGCTCAGTGTGGAGTCTAGNATTAATTTCCACGGTGCCATCGTCTTGTGACTGGAGT 1226
XX
XX QY 115 CAGTAAANNTTGGGGCTCCCGTATGAGATGTCGCCGGGGCAAGGCGCTGGTGTCCACCC 174
XX DB 1225 CGCTCAAAAGCAGACCCGCTCGTCCATGTCGTTGACTATCAGTATGTCCGGCTCCGGCC 1166
XX
XX QY 175 TCGTTTGTGGCG 186
XX DB 1165 TCCACGGTGGCG 1154
XX
RESULT 15

```

ABL27440/c
ID ABL27440 standard; DNA; 6613 BP.
XX
AC ABL27440;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 33793.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEXE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Claim 1: SEQ ID NO 33793; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 6613 BP; 1851 A; 1633 C; 1501 G; 1628 T; 0 U; 0 Other;
Query Match 11.3%; Score 32.8; DB 4; Length 6613;
Best Local Similarity 53.0%; Pred. No. 9;
Matches 70; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
QY 55 CACTATGCAATGTGATCTGGAAACCTGGTTCTTGGGTGGACGCTAGTTATGACTGTGCT 114
Db |||||
3019 CACTGCTCAGTGTGGAGTCTAGAAATATTTCCACGGTGCATCTCTTGTGACTGGAGT 2960
QY 115 CAGTAAATTTGGGGCTCCCGTATGAGATCTCGGGCAAGCGCTCGGTGCCACC 174
Db |||||
2959 CGCTCAAAAGACAGACCCGCTCTCGTCCANGTCGTGACTATCAGTATGTCCTCGGCC 2900
QY 175 TCGTTTGTGGCG 186
Db |||||
2899 TCCAGGTGGCG 2888

Search completed: March 8, 2006, 04:18:55
Job time : 340.308 secs

C	1	260.2.	89.4	1189	15	BT017754	Zea mays
2	259.8.	89.3	320	10	G71239	G71239	Zea mays
3	258.6	88.9	5348	15	S77133	S77133	GRF1=genera
4	220.2	75.7	372	10	G70551	G70551	G71223731FB
5	195.2	67.1	1194	15	BT016497	BT016497	Zea mays
6	183.2	63.0	1082	15	MZEREGP	M96856	Zea mays re
7	144.8	49.8	327	10	BV150852	BV150852	PZA02088-
8	144.8	49.8	338	10	BV150853	BV150853	PZA02088-
9	144.8	49.8	338	10	BV150856	BV150856	PZA02088-
10	144.8	49.8	338	10	BV150858	BV150858	PZA02088-
11	144.8	49.8	338	10	BV150859	BV150859	PZA02088-
12	144.8	49.8	338	10	BV150861	BV150861	PZA02088-
13	144.8	49.8	325	10	BV150863	BV150863	PZA02088-
14	143.8	49.4	328	10	BV150862	BV150862	PZA02088-
15	143.8	49.4	327	10	BV150860	BV150860	PZA02088-
16	139.2	47.8	324	10	BV150855	BV150855	PZA02088-
17	132.8	45.6	334	10	BV150854	BV150854	PZA02088-
18	132.4	45.5	290	10	BV150857	BV150857	PZA02088-

by

61 GCAATGTGATCTGGAACCTGG'

b 311 AGCCGGCTTTATGTGCCTAGAACTAGTAGCTAGTGTT

QV 61 GCAATGTGATCTCGAACCTGGTTCCTCTGGGTCGACGGCT-----AGTATGACATGTC 112

Db 251 GCAATGTGATCTGGAACCTGGTTCTTGGTGGACGCTTGTAGCCGTTATGACTGTC 192
Qy 113 GTCAGTAATAATTTGGGGGCTCCCGATAGAGATGCTGCGGGCAGAGGCTCGGTGTCCA 172
Db 191 GTCCGTAATAATTTGGGGGCTCCCGTAAGGGATGCTGCTGGCAAGGCTCGGTGTCCA 132
Qy 173 CCTCGTTGTGCGGGGGCGCTGGAGCCCGTCTGGTTGGTTGGGTAAGCCCTTTAAAC 232
Db 131 CCTCGTCTGGGGCTGGGGCGCTGAGCCCGTCTGGTTGGTTGGGTAAGCCCTTTAAAC 72
Qy 233 TGTGTGCACTTGCAATTTACCTTTTCCATCGCTGTTATTTAGTGTGCTTATATCAA 291
Db 71 TGTGTGCACTTGCAATTTACCTTTTCCATCGCTGTTATTTAGTGTGCTTATATCAA 13

RESULT 2
G71239 716223731FWo17 maize leaf DNA 320 bp DNA linear STS 08-JUN-2001
LOCUS 716223731FWo17 maize leaf DNA 320 bp DNA linear STS 08-JUN-2001
DEFINITION G71239 716223731FWo17 maize leaf DNA 320 bp DNA linear STS 08-JUN-2001
ACCESSION G71239 716223731FWo17 maize leaf DNA 320 bp DNA linear STS 08-JUN-2001
VERSION G71239.1 GI:14332924
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 320)
AUTHORS Yang, Y.J., Guo, L., Ashlock, D.A., Wen, T.J. and Schnable, P.S.
TITLE 3' UTR sequences of maize genes
JOURNAL Unpublished (2001)
COMMENT

Contact: Schnable, P.S.
Schnable laboratory
Iowa State University
G405 Agronomy Hall, Ames, IA 50011, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
Primer A: GAGCGAGGAGTCTTACAAAG
Primer B: GCGATGGAAGGTAAATGC
PCR Profile:
Denaturation: 94 degrees C for 30 seconds
Annealing: 60 degrees C for 45 seconds
Polymerization: 72 degrees C for 90 seconds
PCR cycles: 31
Thermal cycler: Perkin Elmer TC
Protocol:
Template: 10-20 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/uL
Total vol: 20 uL

Buffer:
MgCl2: 2 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.4.
Location/Qualifiers
1..320
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="DB811"
/db_xref="taxon:4577"
/clone_lib="maize leaf DNA"
/note="PCR products amplified from genomic DNA"
<1..>320

STs
ORIGIN
Query Match 89.3%; Score 259.8; DB 10; Length 320;

Best Local Similarity 99.2%; Pred. No. 1.2e-60;
Matches 261; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AGCCGGCTTTATGCGCTAGAACTAGTAGCTAGTGTGCTGCGAATGACACTAT 60
Db 58 AGCCGGCTTTATGCGCTAGAACTAGTAGCTAGTGTGCTGCGAATGACACTAT 117
Qy 61 GCAATGTGATCTGAACTGCTGTTCTTGGGTGCGACGCTAGTATGACTGTCGTCAGTAA 120
Db 118 GCAATGTGATCTGAACTGCTGTTCTTGGGTGCGACGCTGTTAAGTGTGTCAGTAA 177
Qy 121 AATTGGGGGCTCCCCGATGAGATGCTGCGGGCAAGGCTCGGTGTCACCTCGTTT 180
Db 178 AATTGGGGGCTCCCCGATGAGATGCTGCGGGCAAGGCTCGGTGTCACCTCGTTT 237
Qy 181 GTGGCGGGGGCGCTGAGAGCCCGTCTGGTTGGTTGGGTAAGCCCTTTAACTGTTGCA 240
Db 238 GTGGCGGGGGCGCTGAGAGCCCGTCTGGTTGGTTGGGTAAGCCCTTTAACTGTTGCA 297
Qy 241 CTTGCATTTTACCTTTTCCATCG 263
Db 298 CTTGCATTTTACCTTTTCCATCG 320

RESULT 3
S77133 5348 bp DNA linear PLN 26-SEP-1995
LOCUS S77133 5348 bp DNA linear PLN 26-SEP-1995
DEFINITION GRF1=general regulatory factor [Zea mays, XL80, Genomic, 5348 nt].
ACCESSION S77133
VERSION S77133.1 GI:998429
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 5348)
AUTHORS de Vetten, N.C. and Perl, R.J.
TITLE Two genes encoding GF14 (14-3-3) proteins in Zea mays. Structure,
expression, and potential regulation by the G-box binding complex
JOURNAL Plant Physiol. 106 (4), 1593-1604 (1994)
PUBMED 7846163
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbs 164519] from the original journal article.

FEATURES
source
1..5348
/organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
mRNA join(1491..2583,2671..2749,2876..2998,4387..4503,
4610..4968)
gene 2177..4669
/gene="GRF1"
/note="general regulatory factor"
CDS join(2177..2583,2671..2749,2876..2998,4387..4503,
4610..4669)
/gene="GRF1"
/note="14-3-3 protein homolog"
/codon_start=1
/product="GF14-6"
/protein_id="AA833304.1"
/db_xref="GI:998430"
/translation="MASAELSRENVVMKLAQAERYEEMVEKAVKTVDSSELT
VEENLLSVAYKNVIGARRASWRIISIEQKEGREGNEDVTLIKDYRGKIELSLTKI
CDGILKLETHLPSTAPESKVFYLMKGDYVYLAEFKTGAERKDAENTMWAYKA
AODIALAELAPTHPIRLGLALNFSVFYELNSPDRCASLAKQAFDEAISLDTLSEE
SYKDSLTIMQLLRDNLTLTSDISEDPAEIREAPKEDSSEGG"
ORIGIN

Query Match 88.9%; Score 258.6; DB 15; Length 5348;
Best Local Similarity 94.3%; Pred. No. 2.6e-60;
Matches 282; Conservative 0; Mismatches 9; Indels 8; Gaps 1;


```

/db_xref="taxon:4577"
/clone_lib="Zea mays Mp708"
/dev_stage="seedling"
/notes="Organ: leaf; genomic DNA from inbred line"
<1..>3338

STTS
ORIGIN

Query Match 49.8%; Score 144.8; DB 10; Length 338;
Best Local Similarity 79.4%; Pred. No. 5.6e-29;
Matches 189; Conservative 0; Mismatches 37; Indels 12; Gaps 1;

QY 61 GCAATGTGATCGAACCTGTTCTTGGTGGCGAGCTAGTATGACGTGTC----- 112
Db 1 GCAATGTGATCGAACCTGTTCTTGGTGGCGAGCTAGTATGACGTGTTATGATT 60

QY 113 -----GTCAAGTAAATTTGGGGGCTCCCGTATGAGATGCTGGCGGCAAGGCTCGGTGT 168
Db 1 GCAATGTGATCGAACCTGTTCTTGGTGGCGAGCTAGTATGACGTGTTATGATT 60

QY 229 AAATGTTGTGCTGCTGCTTTACCTTTCCATCGCTGTTATGAGTGGTCTCTAT 286
Db 181 AAATGTTGTGCTGCTGCTTTTAACTTTTCATCGCGTTCAGTGGTCTCTAAATCTAT 238

FEATURES
source
1..338
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="NC7A"
/db_xref="taxon:4577"
/clone_lib="Zea mays NC7A"
/dev_stage="seedling"
/notes="Organ: leaf; genomic DNA from inbred line"
<1..>3338

STTS
ORIGIN

Query Match 49.8%; Score 144.8; DB 10; Length 338;
Best Local Similarity 79.4%; Pred. No. 5.6e-29;
Matches 189; Conservative 0; Mismatches 37; Indels 12; Gaps 1;

QY 61 GCAATGTGATCGAACCTGTTCTTGGTGGCGAGCTAGTATGACGTGTC----- 112
Db 1 GCAATGTGATCGAACCTGTTCTTGGTGGCGAGCTAGTATGACGTGTTATGATT 60

QY 113 -----GTCAAGTAAATTTGGGGGCTCCCGTATGAGATGCTGGCGGCAAGGCTCGGTGT 168
Db 1 GCAATGTGATCGAACCTGTTCTTGGTGGCGAGCTAGTATGACGTGTTATGATT 60

QY 229 AAATGTTGTGCTGCTGCTTTACCTTTCCATCGCTGTTATGAGTGGTCTCTAT 286
Db 181 AAATGTTGTGCTGCTGCTTTTAACTTTTCATCGCGTTCAGTGGTCTCTAAATCTAT 238

RESULT 11
BV150859
LOCUS
DEFINITION
PZA02088-74481-NC7A Zea mays NC7A Zea mays STS genomic, sequence
tagged site.
ACCESSION
BV150859
VERSION
BV150859.1 GI:47100316
KEYWORDS
STS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 338)
McMullen,M.D., Vroh Bi,I., Schultz,L., Duru,N., Schroeder,S.S.,
Sanchez-Villeda,H., Houchins,K., Fang,Z., Polacco,M., Gardiner,J.
and Coe,E.H.Jr.
MMP SNP Discovery
Unpublished (2003)
Contact: Michael D. McMullen
Maize Mapping Project
University of Missouri-Columbia
301 Curtis Hall, Columbia, MO 65211-7020, USA
Tel: 5738827606
Fax: 5738847850
Email: McMullenM@missouri.edu
Primer A: CTATGCAATGATCTGGAACCTG
Primer B: TAAGATGGATGGACACACAAAT
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 uL
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with AmpliTaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.
Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
Contact: Michael D. McMullen
Maize Mapping Project

```


